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(54) Title: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR BIOACTIVE MOLECULES (57) Abstract Degenerate primers which hybridize with various classes of antibiotic biosynthesis gene were used to amplify fragments of DNA from soil and lichen extracts. Cloning and sequencing of the amplified products showed that these products included a variety of novel and previously uncharacterized antibiotic biosynthesis gene sequences, the products of which have the potential to be active as antibiotics, immunosuppressors, antitumor agents, etc. Thus, antibiotic biosynthesis genes can be recovered from soil or lichens by combining a sample with a pair of amplification primers under conditions suitable for polymerase chain reaction amplification, wherein the primer set is a degenerate primer set selected to hybridize with conserved regions of known antibiotic biosynthetic pathway genes, for example Type I and Type II polyketide synthase genes, isopenicillin N synthase genes, and peptide synthetase genes, cycling the combined sample through a plurality of amplification cycles to amplify DNA complementary to the primer set; and isolating the amplified DNA.		

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METHOD FOR ISOLATION OF BIOSYNTHESIS GENES
FOR BIOACTIVE MOLECULES

DESCRIPTION

BACKGROUND OF THE INVENTION

This application relates to a method for the isolation of biosynthesis genes for antibiotics and other bioactive molecules from complex natural sources such as humus, soil and lichens.

5 Antibiotics play an important role in man's efforts to combat disease and other economically detrimental effects of microorganisms. Traditionally, antibiotics have been identified by screening microorganisms, especially those found naturally in soil, for their ability to produce an antimicrobial substance. In some cases, the gene or genes responsible for antibiotic synthesis have then been identified and cloned into producer organisms which
10 produce the antibiotic in an unregulated manner for commercial applications. However, it has been estimated that less than 1% of the microorganisms present in soil are culturable. Torsvik et al., *Appl. Environ. Microbiol.* 56: 782-787 (1990). Thus, much of the genetic diversity potentially available in soil microorganisms is unavailable through traditional techniques.

15 As pathogenic microorganisms become increasingly resistant to known antibiotics, it would, however, be highly desirable to be able to access the reservoir of genetic diversity found in soil, and to facilitate the exploration of new species of antibiotics which may be made by the vast numbers of unculturable organisms found there. It would further be desirable to have access to novel biosynthetic enzymes and the genes encoding such enzymes,
20 which could be used in recombinant organisms for antibiotic production or for *in vitro* enzymatic synthesis of desirable compounds. Thus, it is an object of the present invention to provide a method and compositions for isolating DNA and DNA fragments encoding enzymes relevant to the production of pharmaceutically active molecules such as antibiotic biosynthesis enzymes.

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SUMMARY OF THE INVENTION

We have now identified degenerate primers which hybridize with various classes of antibiotic biosynthesis genes, and have used such primers to amplify fragments of DNA from soil and lichen extracts. Cloning and sequencing of the amplified products showed that these products included a variety of novel and previously uncharacterized antibiotic biosynthesis gene sequences, the products of which have the potential to be active as antibiotics, immunosuppressors, antitumor agents, etc. Thus, antibiotic biosynthesis genes can be recovered from soil by a method in accordance with the present invention comprising the steps of:

- (a) combining a soil-derived sample with a pair of amplification primers under conditions suitable for polymerase chain reaction amplification, wherein the primer set is a degenerate primer set selected to hybridize with conserved regions of known antibiotic biosynthetic pathway genes, for example Type I and Type II polyketide synthase genes, isopenicillin N synthase genes, and peptide synthetase genes;
- (b) cycling the combined sample through a plurality of amplification cycles to amplify DNA complementary to the primer set; and
- (c) isolating the amplified DNA.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, antibiotic biosynthesis genes can be recovered from soil and lichens by a method comprising the steps of:

- (a) combining a humic or lichen-derived sample with a pair of amplification primers under conditions suitable for polymerase chain reaction amplification, wherein the primer set is a degenerate primer set selected to hybridize with conserved regions of an antibiotic biosynthesis gene;
- (b) cycling the combined sample through a plurality of amplification cycles to amplify DNA complementary to the primer set; and
- (c) isolating the amplified DNA.

As used in the specification and claims of this application, the term "humic or lichen-derived sample" encompasses any sample containing the DNA found in lichens or in samples of humic materials including soil, mud, peat moss, marine sediments, and effluvia

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from hot springs and thermal vents in accessible form for amplification, substantially without alteration of the natural ratios of such DNA in the sample. One exemplary form of a humic sample is a sample obtained by performing direct lysis as described by Barns et al., *Proc. Nat'l Acad. Sci. USA* 91:1609-1613 (1994) on a soil sample and then purifying the total DNA extract by column chromatography. Related extraction methods can be applied to the isolation of community DNA from other environmental sources. See, Trevors et al., eds. *Nucleic Acids in the Environment*, Springer Lab Manual (1995). Lichen-derived samples may be prepared from foliose lichens by the method of fungal DNA extraction described by Miao et al., *Mol. Gen. Genet.* 226: 214-223 (1991). Specific non-limiting procedures for isolation of DNA from humic and lichen samples are set forth in the examples herein.

The humic or lichen-derived sample is combined with at least one, and optionally with several pairs of amplification primers under conditions suitable for polymerase chain reaction amplification. Polymerase chain-reaction (PCR) amplification is a well known process. The basic procedure, which is described in US Patent No. 4,683,202 and 4,683,195, which are incorporated herein by reference, makes use of two amplification primers each of which hybridizes to a different one of the two strands of a DNA duplex. Multiple cycles of primer extension using a polymerase enzyme and denaturation are used to produce additional copies of the DNA in the region between the two primers. In the present invention, PCR amplification can be performed using any suitable polymerase enzyme, including Taq polymerase and Thermo Sequenase™.

The amplification primers employed in the method of the invention are degenerate primer sets selected to hybridize with conserved regions of known antibiotic biosynthetic genes, for example Type I and Type II polyketide synthase genes, isopenicillin N synthase genes, and peptide synthetase genes. Each degenerate primer set of the invention includes multiple primer species which hybridize with one DNA strand, and multiple primer species which hybridize with the other DNA strand. All of the primer species within a degenerate primer set which bind to the first strand are the same length, and hybridize with the same target region of the DNA. These primers all have very similar sequences, but have a few bases different in each species to account for the observed variations in the target region. For this reason, they are called degenerate primers.

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Similarly, all of the primers within a degenerate primer set which bind to the second strand are the same length, hybridize with the same target region of the DNA, and have very similar sequences with a few bases different in each species to account for the observed variations in the target region.

5 The degenerate primer sets of the invention are selected to hybridize to highly conserved regions of known antibiotic biosynthesis genes in such a way that they flank a region of several hundred (e.g. 300) or more base pairs such that amplification leads to the selective reproduction of DNA spanning a substantial portion of the antibiotic biosynthesis gene. Selection of primer sets can be made based upon published sequences for classes of
10 antibiotic biosynthesis genes.

For example, for amplification of Type I polyketide synthase genes, we have designed primers based upon the conserved sequences of six beta-ketoacyl carrier protein synthase domains of the erythromycin gene cluster. Donadio et al., *Science* 252: 675-679 (1991); Donadio and Staver, *Gene* 126: 147-151 (1993). These primers have the sequences

15 5'-GC(C/G) (A/G)T(G/C) GAC CCG CAG CG CGC-3' [SEQ ID No. 1]

and

5'-GAT (C/G)(G/A)C GTC CGC (G/A)TT (C/G)GT (C/G)CC-3' [SEQ ID No. 2].

The expected size of the PCR product is 1.2 kilobase pairs. Other degenerate primer sets for Type I and Type II polyketide synthetase genes could be determined from sequence
20 information available in Hutchinson and Fujii, *Ann. Rev. Microbiol.* 49: 201-238 (1995).

Type II polyketide synthase gene clusters are characterized by the presence of chain length factor genes which are arranged at the 3'-end of the ketosynthase genes. Primers were designed based on one conserved region near the 3'-end of the ketosynthase gene and one at the middle portion of the chain length factor gene. The sequences of one suitable set
25 of amplification primers are:

5' CT(C/G)AC(G/C)(G/T)(C/G)GG(C/G)CGIAC(C/G)GC(C/G)AC(C/G)CG-3' SEQ ID No. 3

and

5' GTT(C/G)AC(C/G)GCGTAGAACCA(C/G)GCGAA-3' SEQ ID No. 4

The expected size of the PCR product was 0.5 kilobase pairs. An alternative set of
30 degenerate primers has the sequence

5'-TTCGG(C/G)GGITTCCAG(T/A)(C/G)IGC(C/G)ATG SEQ ID No. 5

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and

5'-TC(C/G)A(G/T)(C/G)AG(C/G)GC(C/G)AI(C/G)GA(C/G)TCGTAICC SEQ ID No. 6.

These primers were designed based upon consensus sequences for the regions flanking the Ksp (chain length factor) genes. The consensus sequences are available from Hutchinson and Fujii, *supra*.

Primers were designed for beta-lactam biosynthetic genes on the basis of the conserved sequences of a number of isopenicillin N synthase genes as described in Aharanowitz et al., *Ann. Rev. Microbiol.* 46: 461-495 (1992). These primers have the sequences

5'-GG(C/G/T) TC(C/G) GG(C/G) TT(C/T) TTC TAC GC-3' [SEQ ID No. 7]

and

5'-CCT (C/G)GG TCT GG(A/T) A(C/G)A G(C/G)A CG-3' [SEQ ID No. 8].

The expected size of the PCR product is 570 base pairs. Other degenerate primer sets could be determined from sequence information available in Jensen and Demain, "Beta-Lactams" in *Genetics and Biochemistry of Antibiotic Production* (L.C. Vining and C. Studdard, eds.), pp 239-268, Butterworth-Heinemann, Newton, MA (1995).

For isolation of peptide synthetase genes, primers based on two of the conserved core sequences within the functional domains of peptide synthetase genes as described by Turgay and Marahiel, *Peptide Res.* 7: 238-241 (1994) were utilized. These primers had the sequence

5'-ATCTACAC(G/C)TC(G/C)GGCAC(G/C)AC(G/C)GGCAAGCC(G/C)AAGGG-3'

SEQ ID No. 9

and

5'-A(A/T)IGAG(T/G)(C/G)ICCICC(G/C)(A/G)(A/G)(G/C)I(A/C)GAAGAA-3'

SEQ ID No. 10

The expected size of the PCR product is 1.2 kilobase pairs.

PCR amplification can also be used for isolating lichen-derived antibiotic biosynthesis genes and gene fragments. For isolation of Type I polyketide synthase genes from lichens, the primer set used was previously described by Keller et al. in *Molec. Appl. to*

Food Safety Involving Toxic Microorganisms, J.L. Richard, ed., pp. 2630277 (1995), and had the following sequences.

5'-MGIGARGCIYTIGCIATGGAYCCICARCARMG

SEQ ID No. 11

and

5'-GGRTCNCIARYTGIGTICCGTICCRTGIGC

SEQ ID No. 12

The expected size of the PCR product is approximately 0.7 to 0.9 kilobases. Actual products evaluated ranged in size from 637 to 809 nucleotides (not including the 61 nt due to the primers).

Once the primers and the sample are cycled through sufficient thermal cycles to selectively amplify antibiotic biosynthetic DNA in the sample (generally around 25 cycles or more), the amplified DNA is isolated from the amplification mixture. Isolation can be accomplished in a variety of ways. For example, the PCR products can be isolated by electrophoresis on an agarose or polyacrylamide gel, visualized with a stain such as ethidium bromide and then excised from the gel for cloning. Primers modified with an affinity binding moiety such as biotin may also be used during the amplification step, in which case the affinity binding moiety can be used to facilitate the recovery. Thus, in the case of biotinylated primers, the amplified DNA can be recovered from the amplification mixture by coupling the biotin to a streptavidin-coated solid support, for example Dynal streptavidin-coated magnetic beads.

It will be appreciated that the DNA obtained as a result of this isolation will not generally be of a single type because of the degeneracy of the primers and the complexity of the initial sample. Thus, although these steps are sufficient to recover antibiotic biosynthesis genes from soil or lichen, it is preferable to further separate and characterize the individual species of amplified DNA.

This further separation and characterization can be accomplished by inserting the amplified DNA into an expression vector and cloning in a suitable host. The specific combination of vectors and hosts will be understood by persons skilled in the art, although bacterial expression vectors and bacterial hosts are generally preferred. Individual clones are then picked and the sequence of the cloned plasmid determined. While random selection has been employed successfully, selection of antibiotic biosynthesis gene-containing clones

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can be facilitated by screening using hybridization with DNA probes based on conserved sequences or by overlay of bacterial clones with an antibiotic-sensitive test strain.

Once the sequence of the cloned DNA is determined, it can be screened against existing libraries of nucleotide and protein sequences for confirmation as an antibiotic biosynthetic gene or gene fragment. Amplified DNA so-identified can be used in several ways. First, the amplified DNA, or distinctive portions thereof, can be used to as probes to screen libraries constructed from humic-derived or lichen DNA to facilitate the identification and isolation of full length antibiotic biosynthetic genes. Once isolated, these genes can be expressed in readily cultivated surrogate hosts, such as a *Streptomyces* species for soil-derived genes or an *Aspergillus* species for lichen-derived genes. General procedures for such expression are known

in the art, for example from Fujii et al., *Molec. Gen. Genet.* 253: 1010 (1996) and Bedford et al., *J. Bacteriol.* 177: 4544-4548 (1995), which are incorporated herein by reference.

Second, amplified DNA which is different from previously known DNA can be used to generate hybrid antibiotic biosynthesis genes using the procedures described by McDaniel et al, *Nature* 375: 549-554 (1995); Stachelhaus et al., *Science* 269: 69-72 (1995); and Stachelhaus et al, *Biochem, Pharmacol.* 52: 177-186 (1996). In these procedures, the novel DNA sequences isolated using the method of the invention are spliced into a known antibiotic gene to provide an expressible sequence encoding a complete gene product.

Using the method of the invention, a number of unique nucleotide sequences have been identified and characterized. The sequences and the biosynthetic polypeptides/proteins for which they encode, given by sequence ID Nos. 13 to 80, are a further aspect of the present invention.

EXAMPLE 1

Total DNA was extracted from soil samples by a direct lysis procedure as described by Barns et al. (1994). The high molecular weight DNA (>20 kb) in the extract was separated on a Sephadex G200 column (Pharmacia, Uppsala, Sweden) as described by Tsai and Olson, *Appl. Environ. Microbiol.* 58: 2292-2295 (1992).

The DNA extract (10-50 ng template DNA) was added to an amplification mixture (total volume 100 µl) containing 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 2 mM

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MgCl₂, 200 µM of each deoxynucleotide triphosphate, 25 pmol of each Type I polyketide primer (Seq ID Nos 1 and 2) and 5.0 units of Taq polymerase (BRL Life Technologies, Gaithersburg, MD). The mixture was then thermally cycled for 30 cycles in a MJ Research PTC-100 thermocycler using the following program:

5 denaturation 93°C 60 seconds
 annealing 60°C 30 seconds
 extension 72°C 90 seconds

10 The PCR products were then electrophoresed in 1% agarose gels and stained with ethidium bromide to visualize the DNA bands. Bands containing PCR product of the expected size were excised from the gel and purified using a Qiaex Gel Extraction kit (Qiagen GmbH). The purified DNA was ligated to pCRII (Invitrogen) to generate a clone library using *E. coli* INVαF competent cells. 18 clones were chosen at random from the library and sequenced using a Taq Dye Terminator Cycle Sequencing Kit and an Applied Biosystem DNA sequencer model 373. The sequencing primers used included the universal M13 (-20)

15 forward primer, the M13 reverse primer and primers designed from the sequence data obtained. DNA sequences were translated into partial amino acid sequences using a software package from Geneworks (Intelligenetics, Inc.) with further manual adjustments and sent to the NCBI database by e-mail at blast@ncbi.nlm.nih.gov for comparison against protein databases. Altschul et al., "Basic Local Alignment Tool", *J. Mol. Biol.* 215: 403-410 (1990).

20 Blast analysis of the 18 clones pointed to 12 unique sequences that were not identical to each other or to published sequences. Seq. ID No. 13 shows the complete DNA sequence of a representative unique clone (Clone ksfs). Seq. ID No. 14 shows the translated amino acid sequence of this clone. The greatest homology as determined by a Blast analysis is indicated to be Type I polyketide synthases. Similar results were obtained on the Blast

25 search of the other 11 unique clones based upon partial sequences which were determined.

EXAMPLE 2

30 The experiment of Example 1 was repeated using isopenicillin N synthase gene primers (Seq ID Nos. 7 and 8). The thermal cycling program was changed to include 60 second extension periods at 72°C, but otherwise the experimental conditions were the same. Twelve clones were picked at random and yielded one unique sequence that was not identical

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to published sequences. The complete sequence of this clone (Clone ipnsfs) is shown in Seq. ID. No. 15 and the translated amino acid sequence in Seq. ID No. 16. The BLAST search indicated greatest homology for this sequence with isopenicillin N synthases.

EXAMPLE 3

The experiment of Example 1 was repeated using peptide synthetase primers (Seq. ID Nos 9 and 10). The amplification mixture was changed to a 50 ul volume containing 10 to 50 ng of template DNA, 20 mM (NH₄)₂SO₄, 74 mM Tris-HCl (pH 8.8), 1.5 mM MgCl₂, 0.01% Tween 20, 200 µM of each deoxynucleotide triphosphate, 25 pmol of each primer, 0.25 % skim milk and 0.4 units of Ultra Therm DNA Polymerase (Bio/Can Scientific, Mississauga, Ontario). The mixture was thermocycled for 30 cycles using the following program:

denaturation 95°C 60 seconds

annealing 52°C 60 seconds

extension 72°C 120 seconds.

Thirty clones containing a 1.2 kb insert have been partially sequenced. The BLAST analysis of the 30 clones pointed to 28 unique sequences that were not identical to each other or to published sequences. Varying degrees of homology to known peptide synthase genes were seen. Seq. ID No. 17 shows the complete DNA sequence of representative clone (ps32). Seq. ID No. 18 shows the translated amino acid sequence of this clone. Based on a Blast search of these sequences, the greatest homology is to a peptide synthase gene such as the pristinamycin synthase gene from *Streptomyces pristinaespiralis* and *Bacillus* sp. peptide synthetase genes such as gramicidin S synthase and surfactin synthetase. Stachelhaus and Marahiel, *FEMS Micro. Letters* 125: 3-14 (1995); Turgay et al., *Mol. Micro* 6: 529-546 (1992).

Sequence ID Nos. 81 to 94 show an additional 7 unique sequences (nucleic acid and translated amino acid sequences) of 1.2 kb PCR products amplified from soil DNA samples using these primers. These sequences have been named ps 2, ps 3, ps 7, ps 10, ps 24, ps 25 and ps 30. The sequences are unique in that they are all different from each other and from ps 32,

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and while they show greatest homology to peptide synthetase sequences in the databases searched by BLAST analysis, they do not match any known sequence. Within each, the conserved motifs (TGD, KIRGXRIEL, NGK) common to peptide synthetase domains as described by Turgay and Marahiel (1994) can be identified. Descriptive information of the clones follows:

Clone ps 2, 1204 bp, with conserved motifs SGD, KIRGFRIEL, NGK, 67% G + C

Clone ps 3, 1178 bp, with conserved motifs TGD, KIRGSRIEL, NGK, 59 % G + C

Clone ps 7, 1222 bp with conserved motifs TGD, KIRGYRIEL, NGK, 55.5 % G + C

Clone ps 10, 1171 bp with conserved motifs TGD, KIRGHRIEL, NLK, 63% G + C

Clone ps 24, 1190 bp with conserved motifs TGD, KIRGHRIAM, NQK, 56 % G + C

Clone ps 25, 1178 bp with conserved motifs TGD, KLRGYRIEL, NDK 68 % G + C

Clone ps 30, 1200 bp with conserved motifs TGD, KVRGFRIEP, NGK, 64.5 % G + C

Clone ps 32, 1172 bp with conserved motifs TGD, KIRGFRIEL, SGK, 67 % G + C

EXAMPLE 4

The experiment of example 1 was repeated using the Type II polyketide synthase primers given by Seq. ID. Nos. 3 and 4. PCR amplification was carried out in a total volume of 50 ul containing 50 ng of soil DNA, 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 2 mM MgCl₂, 200 uM of each deoxynucleotide triphosphate, 25 pmol of each primer and 5.0 units of *Taq* polymerase (BRL Life Technologies, Gaithersburg, MD). The thermal cycling conditions included denaturations at 94°C for 60 seconds, annealing at 58°C for 30 seconds and extensions at 72°C for seconds, repeated for a total of 30 cycles.

PCR amplification yielded products of the expected size of 0.5 kilobase pairs. Sequencing of 18 randomly selected clones revealed the presence of 5 unique sequence that

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were not identical to each other or to published sequences. Seq. ID No. 19 shows the complete DNA sequence of a representative clone (clone clf). The translated amino acid sequence of this clone is shown in Seq. ID. No. 20. In a BLAST search of this DNA sequence against the protein database, the greatest homology is indicated to chain length factor genes of the Type II polyketide synthases.

Example 5

The experiment of Example 1 was repeated using the Type I polyketide synthase primers designed for fungal sequences. (Seq. ID. Nos. 11 and 12) PCR amplifications were carried out with lichen DNA samples from a variety of lichen species representing 11 genera prepared as described in Miao et al. (1991), *supra*.

PCR amplifications were carried out in a total volume of 50 ul containing approximately 10 ng of lichen DNA and 1 unit of *Taq* polymerase in a reaction as per Example 4. The cycling protocol was 30 cycles of denaturation at 95°C for 60 seconds, annealing at 57°C for 2 minutes and extensions at 72°C for 2 minutes.

Forty seven clones with inserts of the expected size have been partially sequenced. The sequences all show homology to Type I fungal polyketide synthase genes but are all distinct from each other and from known sequences. Seq. ID. No. 21 shows the complete DNA sequence of a 637 base pair product amplified from DNA extracted from the lichen *Xanthoparmelia cumberlandia* (clone Xa.cum.6A). The translated amino acid sequence is shown in Seq. ID. No. 22. The greatest homology as determined by Blast analysis is indicated to fungal Type I polyketide synthase genes. Sequence ID Nos. 29 and 30 show the DNA sequence and conceptual amino acid sequence, respectively, for a further clone Xa.cum.6H isolated in this experiment. Sequences of DNA and the corresponding amino acid sequences for seven other lichen samples, *Leptogium corniculatum* (Seq. ID Nos. 31-42), *Parmelia sulcata* (Seq. ID Nos. 43-50); *Peltigera neopolydactyla* (Seq. ID Nos. 51-60); *Pseudocyphellaria anthraxis* (Seq. ID Nos. 61-62); *Siphula ceratites* (Seq. ID. Nos. 63-66); *Thamnolia vermicularis* (Seq. ID Nos. 67-68); and *Usnea florida* (Seq. ID Nos. 69-80). Each of these sequences showed homology by Blast analysis to fungal Type I polyketide synthase.

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EXAMPLE 6

The experiment of Example 5 was repeated on DNA from the lichen *Solorina crocea* using the degenerate peptide synthetase primers of Example 3. Freshly collected lichen (approximately 1.2 g) was washed in running tap water to remove conspicuous soil and field detritus, and then further cleaned under a dissecting microscope. The cleaned sample was then gently shaken in a 50 ml tube containing about 40 ml of 0.2% SDS for at least 30 minutes and rinsed thoroughly with water. Excess surface water was blotted from the washed, hydrated lichen, and the sample was frozen at -80°C for at least 15 minutes then vacuum dried at room temperature for 4 hours. The lichen was ground in liquid nitrogen using a mortar and pestle to produce a lichen powder for use in preparing DNA extracts.

To prepare the DNA extracts, 0.28g of lichen powder was placed into 18 2-ml microfuge tubes, and each aliquot was mixed with 1.25 ml isolation buffer (150 mM EDTA, 50 mM Tris pH 8, 1% sodium lauroyl sarcosine) and extracted for 1 hour at 62°C. The samples were centrifuged for three minutes to pellet cellular debris and a cloudy supernatant was decanted into new microfuge tubes. Each sample of the supernate was mixed with 750 µl 7.5 M ammonium acetate, incubated on ice for 30 minutes and centrifuged for five minutes at 16,000 X g to precipitate proteins. The supernatant fluid was saved in new microfuge tubes and nucleic acids were precipitated with 0.6 volumes of isopropanol overnight at 4°C. Samples were centrifuged for five minutes at 16,000 X g to pellet nucleic acids. The pellets were dissolved in TE containing RNase (18 µg total) at 50°C for 45 minutes. The solutions were then extracted with an equal volume of TE saturated phenol:chloroform (1:1), and again with chloroform. DNA in the aqueous phase was precipitated with 0.1 M sodium acetate and two volumes of ethanol at -20°C for 2 hours, and then pelleted by centrifugation for five minutes at 16,000 X g. The DNA pellet was washed with 75% ethanol, vacuum dried at room temperature for 3 minutes and then dissolved in TE. The final amount of DNA recovered was approximately 70µg according to fluorometric measurement.

Two clones containing the expected 1.2 kb insert were sequenced and found to contain the same sequence shown in Seq. ID. No. 23. Seq. ID. No. 24 shows the translated amino acid sequence. The sequence is distinct, with greatest homology as determined by Blast analysis to the peptide synthase module of the cyanobacterium *Microcystis aeruginosa*.

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EXAMPLE 7

The experiment of example 4 was repeated using the Type II polyketide synthase primers given by Seq. ID. Nos. 5 and 6. Three starting samples were used for recovery of Type II polyketide synthase genes: two uncharacterized strains of *Streptomyces* (strains WEC 68A and WEC 71B) which had been shown to contain Type II polyketide synthase genes, and a soil sample obtained from a forest area near Vancouver, British Columbia. The soil sample was prepared using the basic protocol from Holben et al, *Appl. Environ. Microbiol.* 54: 703- 711 (1988) with variations in parameters such as mix time to adjust for the individual characteristics of the soil samples.

Streptomyces genomic DNA preparations suitable for PCR amplification were prepared from the mycelia harvested from a 50 ml culture in tryptic soy broth (Difco) which had been grown for 3 days at 300 C. The mycelia were collected by centrifugation at 2500 x g for 10 minutes, the pellets were washed in 10% v/v glycerol and the washed pellets were frozen at -200C. The size of the pellets will vary with different strains; for extraction, 1 g samples were suspended in 5 ml TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA) in a 50 ml screw cap Oakridge tube and lysozyme (to 10 mg/ml) and RNase (to 40 ug/g) were added. Following incubation at 300C for 45 min. a drop of each suspension was transferred to a microscope slide, one drop of 10% SDS was added and the suspension was checked for complete clearing and increased viscosity, indicating lysis. Most strains lyse with this incubation time, but incubation in lysozyme may be continued if necessary. (For strains which are very resistant to lysis, small amounts of DNA suitable for PCR amplification may often be prepared on a FastPrep™ instrument as described below.) Following confirmation of sufficient incubation time in lysozyme, 1.2 ml of 0.5 M EDTA, pH 8.0 was added to the suspension and mixed gently then 0.13 ml of 10 mg/ml Proteinase K (Gibco/BRL) solution was added and incubated for 5 min. at 300 C. 0.7 ml of 10% SDS was added, mixed gently by tilting, then incubated again at 300 C for 2 hours. Following lysis, three successive phenol/chloroform extractions were performed by adding a volume equivalent to the aqueous phase each time of a 1:1 mixture of ultrapure Tris buffer saturated phenol (Gibco/BRL) and chloroform. The aqueous phase was recovered each time following centrifugation at 2500 x g for 10 min. in a shortened (i.e.wide bore) Pasteur pipet to minimize shearing; DNA was precipitated from the final aqueous phase with the addition of 0.1 volume of 3M Na acetate,

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pH 4.8 and 1 volume of isopropanol at room temperature. DNA was spooled from the solution onto a sealed Pasteur pipet, rinsed in ice cold 70% ethanol and solubilized in 0.5 ml TE buffer overnight at room temperature. DNA yields (as determined spectrophotometrically) typically range from 1 to 3 mg from 1 g of mycelia.

5 An alternative method for the preparation of small amounts of *Streptomyces* DNA suitable for PCR amplification has been found to be useful for strains resistant to lysis or when a faster method is desirable. This method makes use of the FastPrep™ instrument (Savant) and the methods and kit supplied by BIO 101 (Bio/Can Scientific, Mississauga, Canada). A 2 ml aliquot from a 20 ml, 3 day culture in tryptic soy broth is pelleted in a 2 ml
10 microfuge tube and the size of the mycelial pellet is estimated. "Small" pellets are resuspended in 100 ul of sterile distilled water; larger pellets are resuspended in 200-300 ul of water. 200 ul of suspension is transferred to a homogenization tube from the kit. Following the manufacturer's protocol for the preparation of DNA from medium hard tissue, the large bead is added to this tube (which already contains a small bead) and 1 ml of solution CLS-TC
15 from the kit is added and the samples are processed in the instrument for 10 seconds at speed setting 4.5. Samples are then spun 15 min. at 10,000 x g at 40C and 600 ul of the supernatant is transferred to a clean microfuge tube, 400 ul of Binding Matrix is added and mixed gently, then the sample is spun for 1 min. as above. The supernatant is discarded while the pellet is resuspended in 500 ul SEWS-M and transferred to a SPIN™ Filter unit. This is spun for 1
20 minute, the contents of the catch tube are discarded and the unit is spun again to dry. The filter unit is transferred to a new microfuge tube and DNA is eluted from the matrix in 100 ul DES which is left on the filter for 2-3 min. at room temperature. Eluted DNA is collected by spinning once again and this DNA is now ready to use in PCR amplifications. Due to components of the final solution, DNA prepared by this method is difficult to quantify.
25 Typically 1 ul or 1/10 ul of this eluate is suitable as a template for PCR; larger quantities may be inhibitory to the PCR polymerase.

 PCR amplification was carried out in a total volume of 50 ul containing 50 ng of DNA, 5 % DMSO, 1.25 mM MgCl₂, 200 uM of each deoxynucleotide triphosphate, 0.5 ug of each primer and 5.0 units of *Taq* polymerase (BRL Life Technologies, Gaithersburg, MD).

30 The thermal cycling started with a 'touch-down' sequence, lowering the annealing temperature from 65°C to 58°C over the course of 8 cycles. The temperature of the annealing step

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was then maintained at 58°C for a further 35 cycles. The overall cycle used was: denaturation at 94°C for 45 seconds, annealing at 65°C to 58°C for 1 minute and extension at 72°C for 2 minutes. The size of the amplified fragments was expected to be approximately 1.5 kb.

Amplification of the two *Streptomyces* strains produced DNA fragments of the expected size (1482 bp and 1538 bp). Open reading frame analysis of the two sequences revealed the presence of a set of three ORFs each, corresponding to the 3'-ends of the putative Ks_{α} -subunit genes (50 to 60 bp), possible full-length Ks_{β} genes (approx. 1.2 kb) and the first halves of potential ACP genes (approx 100 bp). In each sequence, the first and second ORFs were linked by a stop codon overlap typical of $Ks_{\alpha,\beta}$ gene pair junctions and a possible indication of tight coexpression through translational coupling. The two Ks_{β} genes were separated from the downstream ACP genes by a short spacer, again consistent with the expected gene organization.

Two clones were selected from among clones created using the soil DNA as a source which were found to produce 1.5 kb inserts. These inserts were sequenced and found to exhibit similarity to known KS_{β} genes with three ORFs as described above. The translated amino acid sequences of the four genes are shown in Sequence ID Nos 25 to 28.

The four putative KS_{β} genes had G+C content over 70% which is typical for the coding regions of Actinomycete genes. Results of data base searches established that the deduced products of all four ORFs were similar to known KS_{β} gene products from Type II polyketide synthases but they did not match any known sequences.

EXAMPLE 8

DNA can be extracted from large volumes of soil in accordance with the following procedure. Place dry soil into a sterile blender with 0.2% sodium pyrophosphate (100 ml/100 grams of soil). The pH of the sodium pyrophosphate solution should be about 10, although some variation to account for the characteristics of the soil may be appropriate. The mixture is blended for 30 seconds, decanted into centrifuge bottles and then centrifuged for 15 minutes at 100 X g at 4°C. The supernatant is decanted, filtered two times through cheese cloth and saved. The pelleted soil is extracted an additional two times using the same procedure.

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After the extractions, the pooled supernatants are centrifuged for 15 minutes at 10,500 X g and the pellets are collected. The pellet may be incubated for 6 hours at 55°C in pre-germination medium (0.5% w/v yeast extract (Difco), 0.5% w/v casamino acids (Difco) with 0,005 M CaCl₂ and 0.025 M TES, pH 8.0 (added separately from sterile stock after autoclaving other components)) and then repelleted, or it may be used directly. In either case, the pellet (approximately 30-200 mg) is mixed with 5 ml 1X TE (pH 8.0), 500 µl 0.5M EDTA (pH 8.0) and 500 µl - 20 mg/ml lysozyme in 1X TE (pH 8.0) and incubated for 30 minutes at 37°C. 500 µl of 20% SDS and 100 µl - 1% proteinase K in TE and 1% SDS are then added and the mixture is vortexed gently before incubating for 60 minutes at 55°C or overnight at 37°C.

The incubated mixture is combined with 10 ml 20% polyvinylpyrrolidone (avg. MW=40,000) and incubated for 10 minutes at 70°C. One-half volume of 7.5 M ammonium acetate (stored at -20°C) is then added, the resulting mixture is placed for 10 minutes on a low speed shaker, and then centrifuged for 20 minutes at 18,500 X g. The supernatant is combined with 1 volume of isopropanol and incubated for 30 minutes at -20°C before centrifuging for 20 minutes at 18,500 X g. The pellet from this centrifugation is washed in 70% ethanol, and centrifuged for 10 minutes at 18,500 X g. The pellet from this final centrifugation is collected and air dried.

EXAMPLE 9

To extract DNA from small amounts of soil the following procedure can be used. Combine soil (approx 1 g) with 1 ml distilled water, vortex to suspend and pellet at 19,000 X g for 5 minutes. After removing the supernatant, freeze/thaw the samples twice by either of the following techniques (a) -20°C freezer, 30 minutes, followed by 50-60°C water bath (2 minutes), repeated 2 times; or (b) quick freeze in EtOH-dry ice bath (dip in until frozen, approx one minute) followed by 60°C water bath (2 minutes), repeated 2 times. The pellets are then suspended in 350 µl TE buffer (pH 8.0), 50 µl 0.5 M EDTA and 50 µl-20 mg/ml lysozyme in TE buffer, vortexed and incubated at 37°C for 30 minutes in a water bath. 50 µl of 20% SDS and 10 µl 1% Proteinase K/ 1% SDS in TE buffer is added, vortexed, and incubated for one hour at 55°C or overnight at 37°C. One-tenth volume of 20% polyvinylpyrrolidone (avg. MW=40,000) is then added and incubated at 70°C for 10 minutes.

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One-half volume of 7.5 M ammonium acetate (stored at -20°C) is added, the tubes are shaken at low speed for ten minutes and then centrifuged at 19,000 X g for 20 minutes. The supernatant is collected using pipets with cut tips to avoid shearing DNA, combined with one volume of isopropanol, mixed gently, and stored at -20°C for 30 minutes or 4°C overnight.

- 5 The DNA is then collected as a pellet by centrifugation at 19,000 X g for 10 minutes. The resulting pellet is washed with 0.5 ml of 70% ethanol (stored at -20°C) and then air or vacuum dried. The dried DNA is then dissolved in 50-150 ul of TE buffer, incubated at 4°C for one hour and then heated to 60°C for 10 minutes to facilitate dissolving DNA. The resulting solutions are stored at -20°C until use.

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SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Terragen Diversity Inc.
 - (ii) TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR BIOACTIVE MOLECULES
 - (iii) NUMBER OF SEQUENCES: 94
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Deeth Williams Wall
 - (B) STREET: National Bank Building, 150 York Street, Suite 400
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3S5
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 - (B) COMPUTER: Dell (IBM Compatible)
 - (C) OPERATING SYSTEM: Windows 95
 - (D) SOFTWARE: Word 97
 - (vi) CURRENT APPLICATION DATA :
 - (A) APPLICATION NUMBER: Not yet assigned
 - (B) FILING DATE: May 21, 1998
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/861,774
 - (B) FILING DATE: May 22, 1997
 - (viii) ATTORNEY/AGENT INFORMATION :
 - (A) NAME: Eileen McMahon
 - (B) REGISTRATION NUMBER:
 - (C) REFERENCE/DOCKET NUMBER: 1694/0005
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 416-941-9440
 - (B) TELEFAX: 416-941-9443
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: yes
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
GCSRTSGACC CGCAGCGCGC 20
- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GATSRCGTCC GCRTTSGTSC C 21

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
CTSACSKSGG SCGNACSGCS ACSCG 25

(2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
GTTSACSGCG TAGAACCASG CGAA 25

(2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
TTCGGSGGNT TCCAGWSNGC SATG 24

(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA

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(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TCSAKSAGSG CSANSGASTC GTANCC 26

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GGBTCSSGGST TYTCTACGC 20

(2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
CCTSGGTCTG GWASAGSACG 20

(2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
ATCTACACST CSGGCACSAC SGGCAAGCCS AAGGG 35

(2) INFORMATION FOR SEQ ID NO:10:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

- 21 -

AWNGAGKSN CICCRRSNM GAAGAA 26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

MGIGARGCIY TIGCIATGGA YCCICARCAR MG 32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGRTCNC CIA RYTGIGTICC IGTICCRTGI GC 32

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1206

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGGTGGACC	CGCAGCAGCG	CCTCATGCTG	GAGCTGGCCT	GGTCCGCGCT	50
GGAAAGCGCA	GGTCATCCGC	CCTCGATATT	CCCCGGCCTG	ATCGGGGTCT	100
ATGTGCGCAT	GAAGTGAAT	CGCTATCGCG	CGAATTGCAT	TTCTGCACAC	150
CCTGATGTGG	TGGAGCGATT	CGGTGAATTG	AACACAGCGC	TCGCCAACGA	200
ATACGACTTT	CTTGCTACCC	GAATCTCCTA	CAAGCTCAAT	CTGCGCGGTC	250
CCAGCGTCAC	TATCAGCACC	GCTTGTTTGA	CTTCCCTGGT	TGCCATTGCT	300
CAGGCTTCGC	AGGCGTTGCT	CAACTATGAA	TGCGACATTG	CTTTGGCTGG	350
GGTTGCCTCC	ATAACCGTGC	CTGTCAATGC	AGGCTACCTC	TACCAAGAAA	400
GGTGGCATGC	TTTCACCGAA	GGGCATTGTC	CTACATTGCA	TGCCCCAGCA	450
CGGGACCACT	TCAATGATGC	CCCCTGTCTC	CTTTTTCGGG	GCCTGGAAAA	500
CCCATCCAGG	AGGGGGGGGG	GGGCCCTCAT	ACCCGGCCTT	TCAAGCGGGA	550
ACCTCTCACA	GGAAGCGGAT	GTTTCAGCCG	AAGGGATGTT	GAACATTGAC	600
GCCGGCAGCA	CGGGGGACAA	GTTTCAGGGAT	GGGCGCGCTT	TTGTTGTATG	650
GGGGGGGCCT	GGAAGAAGCA	TTCAAGGGAC	GGTGATCAAA	CTTAACCCCT	700
TCATTGCGCG	GTTTGCCGCG	GAACAAGGAC	GGGTTCGGAC	AAGGCGAGTT	750
TACCGGCGCC	CAGGCGTCAA	TGGTCAGGGC	GGAGTTCATT	TCGCTTTGGC	800

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GGTGGAGTTT	GCGGGATATT	CGAATCCCGC	AAGCATCGGG	ATTTTCATTTCG	850
AAAACCCACG	GGCACGGGCG	ACGCCATTGG	GCGATCCGAT	AGAAGTGGCC	900
GCGCTAAAGA	TGGTTTTTCG	CCGACGCTCG	TTCCAGAGGC	GCCGTTGCGC	950
CCTTGGATCG	GTCAAGAGTT	GTGTCGGACA	CCTGGTTCAC	GCCGCCGGCG	1000
TGACCGGATT	TATCAAGGCT	GTCTTGTCGG	TCTACCACGG	CAAGATCGCA	1050
CCGACACTGT	TTTTTCGAGAA	AGCAAATCCG	AGGCTCGGGC	TGGAAGACAG	1100
TCCTTTCTAT	GTCAATGCCG	GACTCGAGAA	GTGGACGGCC	GCCGAGCAGC	1150
CACGCCGCGC	GGGGGTCAGT	GCTTTCGGGG	TCGGTGGCAC	CAATGCGCAC	1200
GCGATC					1206

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Val	Asp	Pro	Gln	Gln	Arg	Leu	Met	Leu	Glu	Leu	Ala	Trp	Ser	5	10	15
Ala	Leu	Glu	Ser	Ala	Gly	His	Pro	Pro	Ser	Ile	Phe	Pro	Gly	Leu	20	25	30
Ile	Gly	Val	Tyr	Val	Gly	Met	Asn	Trp	Asn	Arg	Tyr	Arg	Ala	Asn	35	40	45
Cys	Ile	Ser	Ala	His	Pro	Asp	Val	Val	Glu	Arg	Phe	Gly	Glu	Leu	50	55	60
Asn	Thr	Ala	Leu	Ala	Asn	Glu	Tyr	Asp	Phe	Leu	Ala	Thr	Arg	Ile	65	70	75
Ser	Tyr	Lys	Leu	Asn	Leu	Arg	Gly	Pro	Ser	Val	Thr	Ile	Ser	Thr	80	85	90
Ala	Cys	Ser	Thr	Ser	Leu	Val	Ala	Ile	Ala	Gln	Ala	Ser	Gln	Ala	95	100	105
Leu	Leu	Asn	Tyr	Glu	Cys	Asp	Ile	Ala	Leu	Ala	Gly	Val	Ala	Ser	110	115	120
Ile	Thr	Val	Pro	Val	Asn	Ala	Gly	Tyr	Leu	Tyr	Gln	Glu	Arg	Trp	125	130	135
His	Ala	Phe	Thr	Glu	Gly	His	Cys	Pro	Thr	Phe	Asp	Ala	Pro	Ala	140	145	150
Arg	Asp	His	Phe	Asn	Asp	Ala	Pro	Cys	Leu	Leu	Phe	Ala	Gly	Leu	155	160	165
Glu	Asn	Pro	Ser	Arg	Arg	Gly	Gly	Gly	Ala	Leu	Ile	Pro	Gly	Leu			

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	170		175		180
Ser Ser Gly Asn	Leu Ser Gln Glu Ala	Asp Val Ser Ala Glu Gly			
	185	190			195
Met Leu Asn Ile	Asp Ala Gly Ser Thr	Gly Asp Lys Phe Arg Asp			
	200	205			210
Gly Arg Ala Phe	Val Val Trp Gly Gly	Pro Gly Arg Ser Ile Gln			
	215	220			225
Gly Thr Val Ile	Lys Leu Asn Pro Phe	Ile Gly Gly Phe Ala Ala			
	230	235			240
Glu Gln Gly Arg	Val Arg Thr Arg Arg	Val Tyr Arg Arg Pro Gly			
	245	250			255
Val Asn Gly Gln	Gly Gly Val His Phe	Ala Leu Ala Val Glu Phe			
	260	265			270
Ala Gly Tyr Ser	Asn Pro Ala Ser Ile	Gly Ile Ser Phe Glu Asn			
	275	280			285
Pro Arg Ala Arg	Ala Thr Pro Leu Gly	Asp Pro Ile Glu Val Ala			
	290	295			300
Ala Leu Lys Met	Val Phe Arg Arg Arg	Ser Phe Gln Arg Arg Arg			
	305	310			315
Cys Ala Leu Gly	Ser Val Lys Ser Cys	Val Gly His Leu Val His			
	320	325			330
Ala Ala Gly Val	Thr Gly Phe Ile Lys	Ala Val Leu Ser Val Tyr			
	335	340			345
His Gly Lys Ile	Ala Pro Thr Leu Phe	Phe Glu Lys Ala Asn Pro			
	350	355			360
Arg Leu Gly Leu	Glu Asp Ser Pro Phe	Tyr Val Asn Ala Gly Leu			
	365	370			375
Glu Lys Trp Thr	Ala Ala Glu Gln Pro	Arg Arg Ala Gly Val Ser			
	380	385			390
Ala Phe Gly Val	Gly Gly Thr Asn Ala	His Ala Ile			
	395	400			

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

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(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCCGGGT	TTTTCTACGC	GTCCAACCAC	GGGATCGACG	TCACGCGGGT	50
GCGCGACGAG	GTGAACAAGT	TCCACGCCGA	GATGACGCCC	GGGGAGAAGT	100
TCGAGCTGGC	CATCAACGCC	TACAACGACG	CGAATCCGCA	TACCCGCAAC	150
GGGTATTACA	TGGCCGTCGA	AGGCAAGAAG	GCCGTCGAGT	CCTTCTGCTA	200
CCTCAACCCG	GCCTTCACCC	CCGAGCACCC	GATGATCGAG	GCGGGCGCGG	250
CGGGGCACGA	GGTGAACAAC	TGGCCGGACG	AGGCTCGCCA	CCCCGGCTTC	300
CGTGAGTACG	GGGGAGCAGT	ACTTCGAAGA	GGATCCTCCG	ACCTGTCACT	350
GGTGCTGCTG	CGTGGGTACG	CGCTGGCCCT	GGGCAAGGAC	GAGAACTACT	400
TCGACGACTA	CGTCAAGCAC	TCCGACACGC	TCTCGGCCGT	CTCGCTGATC	450
CGTTACCCGT	ACCTGGAGAA	CTACCCGCCG	GTGAAGACCG	GTCCGGACGG	500
CGAGAAGCTC	AGCTTCGAGG	ATCACTTCGA	CGTCTCGCTG	ATCACCGTGC	550
TCTTCCAGAC	CCAGG				565

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly	Ser	Gly	Phe	Phe	Tyr	Ala	Ser	Asn	His	Gly	Ile	Asp	Val	Thr	
				5					10					15	
Arg	Val	Arg	Asp	Glu	Val	Asn	Lys	Phe	His	Ala	Glu	Met	Thr	Pro	
				20					25					30	
Gly	Glu	Lys	Phe	Glu	Leu	Ala	Ile	Asn	Ala	Tyr	Asn	Asp	Ala	Asn	
				35					40					45	
Pro	His	Thr	Arg	Asn	Gly	Tyr	Tyr	Met	Ala	Val	Glu	Gly	Lys	Lys	
				50					55					60	
Ala	Val	Glu	Ser	Phe	Cys	Tyr	Leu	Asn	Pro	Ala	Phe	Thr	Pro	Glu	
				65					70					75	
His	Pro	Met	Ile	Glu	Ala	Gly	Ala	Ala	Gly	His	Glu	Val	Asn	Asn	
				80					85					90	
Trp	Pro	Asp	Glu	Ala	Arg	His	Pro	Gly	Phe	Arg	Glu	Tyr	Gly	Gly	
				95					100					105	
Ala	Val	Leu	Arg	Arg	Gly	Ser	Ser	Asp	Leu	Ser	Leu	Val	Leu	Leu	
				110					115					120	
Arg	Gly	Tyr	Ala	Leu	Ala	Leu	Gly	Lys	Asp	Glu	Asn	Tyr	Phe	Asp	
				125					130					135	
Asp	Tyr	Val	Lys	His	Ser	Asp	Thr	Leu	Ser	Ala	Val	Ser	Leu	Ile	

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	140		145		150
Arg Tyr Pro Tyr	Leu Glu Asn Tyr Pro	Pro Val Lys Thr Gly	Pro		
	155		160		165
Asp Gly Glu Lys	Leu Ser Phe Glu Asp	His Phe Asp Val Ser	Leu		
	170		175		180
Ile Thr Val Leu	Phe Gln Thr Gln				
	185				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1172

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGGAGGGGC	CGCCCGGGGC	GAAGAAGCTG	TCCGTCCGAC	TGACACGTTC	50
CACTCCGAGG	AGCCCGGACC	AGATGCGCGC	CAGCTTTACC	TCGACCGGCG	100
TAGATGGCGG	GTCTAGTCA	GTGCGATCCG	ATGAGTCATC	TGGAGGTGCA	150
GGCAGCACCT	TCAGATCGAT	CTTGCCGCTC	GCCATGCGCG	GCATCTCGCG	200
GAGCTCGACG	AATGCAGCCG	GAATCATGTA	CTCGGGCAAC	CGCGTGCGAA	250
GATGATCGCG	CAGCTCGGAC	GCGGCGACCG	AGGCGAGCCG	AGGCGACCAG	300
TACGCAACGA	GACGCTTGTC	GCCGGCCCCG	TCCTGCCGCG	CCAGGACGAC	350
GGCCGTCTCG	ACACCGGGGT	GATCGGCCAG	CGCCGCCTCG	ATCTCACCAG	400
GCTCGATGCG	GAAGCCGCGG	ATCTTGACCT	GATGATCCGC	GCGCCCGATG	450
AAGTCGAGGT	TGCCGTCCGG	AAGCCAGCGC	ACCAGGTCGC	CGGTCCGGTA	500
CAGCCGCGAG	CCAGGTGCAC	CGAATGGATC	GGGTACGAAC	CGCGCTCCGG	550
TGAGGGCGGC	ATCATCGACA	TAGCCGCGCG	CGAGGTTCTC	GCCACCGATG	600
TACAGTCTCG	CGATCACGCG	CGCCGGAACG	GGCTCGAGTG	CGCTATCGAG	650
CACGTAGACC	TGAACGTTGT	CGAGCGGACG	GCCGATCGAC	GGCAGCTCGG	700
ACCCGTGTTT	GGACGCGGGC	GACACGATCG	CCCACGTCGT	ATCGACCGCG	750
TTCTCCGTCG	GGCCGTACTC	GTTGAGCATG	CGGTAGTGCG	CATCGCGCGG	800
TGGACGCCGC	GTGAGTCGAT	CACCGCCCGT	ACGCAGCACG	CGCAACGAGC	850
GTGGAAAGTC	GCCAGCCGCG	AGCAACGCGT	CGAGTAGCCG	GCCTGGAAGA	900
TCGGAGATCG	TGATCCCCCA	TCGCGTCAGG	TTCTCGAGCA	GGCGCGGCGG	950
ATCGAGGCGG	AGCTCGTTGT	CCACCAGATG	AAGCCGGGCG	CCCGTCGCCA	1000
GCGTGGACCA	CAGCTCGAGC	GCCGCGGCAT	CGAACGACAT	CGAGTAGATC	1050
TGCGTCACGC	GGTCGTCGGC	ACTGATCTCG	ACGGCACGCT	GGTTCCACGC	1100
GATCAAATTT	CTCAGTGCAC	GGTGCGGCAC	GGCGACGCCC	TTCGGCTTGC	1150
CCGTCGTGCC	CGACGTGTAG	AT			1172

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

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(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile	Tyr	Thr	Ser	Gly	Thr	Thr	Gly	Lys	Pro	Lys	Gly	Val	Ala	Val	5	10	15
Pro	His	Arg	Ala	Leu	Arg	Asn	Leu	Ile	Ala	Trp	Asn	Gln	Arg	Ala	20	25	30
Val	Glu	Ile	Ser	Ala	Asp	Asp	Arg	Val	Thr	Gln	Ile	Tyr	Ser	Met	35	40	45
Ser	Phe	Asp	Ala	Ala	Ala	Leu	Glu	Leu	Trp	Ser	Thr	Leu	Ala	Thr	50	55	60
Gly	Ala	Arg	Leu	His	Leu	Val	Asp	Asn	Glu	Leu	Arg	Leu	Asp	Pro	65	70	75
Pro	Arg	Leu	Leu	Glu	Asn	Leu	Thr	Arg	Trp	Gly	Ile	Thr	Ile	Ser	80	85	90
Asp	Leu	Pro	Gly	Arg	Leu	Leu	Asp	Ala	Leu	Leu	Ala	Ala	Gly	Asp	95	100	105
Phe	Pro	Arg	Ser	Leu	Arg	Val	Leu	Arg	Thr	Gly	Gly	Asp	Arg	Leu	110	115	120
Thr	Arg	Arg	Pro	Pro	Arg	Asp	Ala	His	Tyr	Arg	Met	Leu	Asn	Glu	125	130	135
Tyr	Gly	Pro	Thr	Glu	Asn	Ala	Val	Asp	Thr	Thr	Trp	Ala	Ile	Val	140	145	150
Ser	Pro	Ala	Ser	Glu	His	Gly	Ser	Glu	Leu	Pro	Ser	Ile	Gly	Arg	155	160	165
Pro	Leu	Asp	Asn	Val	Gln	Val	Tyr	Val	Leu	Asp	Ser	Ala	Leu	Glu	170	175	180
Pro	Val	Pro	Ala	Arg	Val	Ile	Gly	Glu	Leu	Tyr	Ile	Gly	Gly	Glu	185	190	195
Asn	Leu	Ala	Arg	Gly	Tyr	Val	Asp	Asp	Ala	Ala	Leu	Thr	Gly	Ala	200	205	210
Arg	Phe	Val	Pro	Asp	Pro	Phe	Gly	Ala	Pro	Gly	Ser	Arg	Leu	Tyr	215	220	225
Arg	Thr	Gly	Asp	Leu	Val	Arg	Trp	Leu	Pro	Asp	Gly	Asn	Leu	Asp	230	235	240
Phe	Ile	Gly	Arg	Ala	Asp	His	Gln	Val	Lys	Ile	Arg	Gly	Phe	Arg	245	250	255
Ile	Glu	Leu	Gly	Glu	Ile	Glu	Ala	Ala	Leu	Ala	Asp	His	Pro	Gly			

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260	265	270
Val Glu Thr Ala	Val Val Leu Ala Arg	Gln Glu Arg Ala Gly Asp
275	280	285
Lys Arg Leu Val	Ala Tyr Trp Ser Pro	Arg Leu Ala Ser Val Ala
290	295	300
Ala Ser Glu Leu	Arg Asp His Leu Arg	Thr Arg Leu Pro Glu Tyr
305	310	315
Met Ile Pro Ala	Ala Phe Val Glu Leu	Arg Glu Met Pro Arg Met
320	325	330
Ala Ser Gly Lys	Ile Asp Leu Lys Val	Leu Pro Ala Pro Pro Asp
335	340	345
Asp Ser Ser Asp	Arg Thr Asp Tyr Asp	Pro Pro Ser Thr Pro Val
350	355	360
Glu Val Lys Leu	Ala Arg Ile Trp Ser	Gly Leu Leu Gly Val Glu
365	370	375
Arg Val Ser Arg	Thr Asp Ser Phe Phe	Ala Pro Gly Gly Pro Ser
380	385	390

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

TTCGGCGGGT TCCAGACGGC CATGGTGCTG ACGACGGGAC GGGACAATGA 50
GAAGTAGCGT CGCGGTCACC GGCATCGGCC TGGTGGCCGC CAACGGGCTC 100
ACCACCGAGG ACGTGTGGTC GGCCGTGCTC GCGGGCCGCA GCGGCCTTGG 150
AACGATCACC CGTTTCGACG CCGCGGGCTA CCCGGCCCGG ATCGCCGGCG 200
AGGTGTCGCA GTTCGTGGCC GAGGAGCACA TCGCCGACCG GCTGATCCCG 250
CAGACCGACC ACATGACCCG GCTGGCGCTG GCCGCGGCCG AGTCGGCGAT 300
CCGGGACGCC AAGGTGGGAC CTGGCCGAGC TGCCCGATTC GGCGCGGGCG 350
TGGTCACCGC CGCGACGGCA GGCGGCTTCG AGTTCGGCCA GCGGGAGCTG 400
GAGAACCTGT GGCGCAAGGG GCCTGAGCAC GTCAGCCCCT ACCAGTCCTT 450
CGCCTGGTTC TACGCCGTCA AC

```

472

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE:
 (A) DESCRIPTION: protein
 (iii) HYPOTHETICAL: no
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Arg Ser Ser Val Ala Val Thr Gly Ile Gly Leu Val Ala Ala
      5                      10                      15
Asn Gly Leu Thr Thr Glu Asp Val Trp Ser Ala Val Leu Gly Gly
      20                      25                      30
Arg Ser Gly Leu Gly Thr Ile Thr Arg Phe Asp Ala Ala Gly Tyr
      35                      40                      45
Pro Ala Arg Ile Ala Gly Glu Val Ser Gln Phe Val Ala Glu Glu
      50                      55                      60
His Ile Ala Asp Arg Leu Ile Pro Gln Thr Asp His Met Thr Arg
      65                      70                      75
Leu Ala Leu Ala Ala Ala Glu Ser Ala Ile Arg Asp Ala Lys Val
      80                      85                      90
Gly Pro Gly Arg Ala Ala Arg Phe Gly Ala Gly Val Val Thr Ala
      95                      100                     105
Ala Thr Ala Gly Gly Phe Glu Phe Gly Gln Arg Glu Leu Glu Asn
      110                     115                     120
Leu Trp Arg Lys Gly Pro Glu His Val Ser Pro Tyr Gln Ser Phe
      125                     130                     135
Ala Trp Phe Tyr Ala Val Asn
      140

```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no

- (iv) ANTI-SENSE: no

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

TATATTACTC CAGGTTGCTT ACGAAGCATT GGAGATGTCC GGATATTTTCG      50
CCGATTCGTC CAGGCCTGAG GATGTCGGTT GCTATATTGG AGCTTGTGCA      100
ACAGATTACG ATTTCAACGT AGCATCCCAT CCTCCACGG CGTATTCAGC      150
GACTGGCACG CTCCGATCTT TTCTAAGTGG CAAGCTGTCC CATTACTTTG      200
GTTGGTCCGG TCCCTCTCTT GTCCTAGACA CTGCCTGCTC TTCGTCGGCG      250
GTGGCTATTC ATACTGCATG TACTGCTTTG AGGACTGGCC AGTGTTCCTCA      300
AGCTCTAGCA GCGGGGATCA CGTTGATGAC AAGCCCGTAT CTCTATGAGA      350
ACTTCTCTGC AGCCCATTTT TTAGTCCAA CGGGAGGTTT AAAGCCGTTT      400

```

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```

AGCGCAGRTG CAGATGGATA CTGTAGAGGA GAAGGTGGTG GCCTCGTGGT 450
CTTGAAACGA CTTTCAGATG CTCTCAGGGA TGATGACCAT ATTATTAGTG 500
TCATCGCTGG CTCGGCGGTC AACCAGAACG ACAACTGCGT GCCTATCACC 550
GTCCCTCACA CTTTCGTCTCA GGGAAATCTC TATGAACGAG TTACCAGACA 600
GGCAGGGGTG ACACCCAATA AAGTCACTTT TGTGGAA 637

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Ile Leu Leu Gln Val Ala Tyr Glu Ala Leu Glu Met Ser Gly Tyr
      5                      10                      15
Phe Ala Asp Ser Ser Arg Pro Glu Asp Val Gly Cys Tyr Ile Gly
      20                      25                      30
Ala Cys Ala Thr Asp Tyr Asp Phe Asn Val Ala Ser His Pro Pro
      35                      40                      45
Thr Ala Tyr Ser Ala Thr Gly Thr Leu Arg Ser Phe Leu Ser Gly
      50                      55                      60
Lys Leu Ser His Tyr Phe Gly Trp Ser Gly Pro Ser Leu Val Leu
      65                      70                      75
Asp Thr Ala Cys Ser Ser Ser Ala Val Ala Ile His Thr Ala Cys
      80                      85                      90
Thr Ala Leu Arg Thr Gly Gln Cys Ser Gln Ala Leu Ala Gly Gly
      95                      100                     105
Ile Thr Leu Met Thr Ser Pro Tyr Leu Tyr Glu Asn Phe Ser Ala
      110                     115                     120
Ala His Phe Leu Ser Pro Thr Gly Gly Ser Lys Pro Phe Ser Ala
      125                     130                     135
Xaa Ala Asp Gly Tyr Cys Arg Gly Glu Gly Gly Gly Leu Val Val
      140                     145                     150
Leu Lys Arg Leu Ser Asp Ala Leu Arg Asp Asp Asp His Ile Ile
      155                     160                     165
Ser Val Ile Ala Gly Ser Ala Val Asn Gln Asn Asp Asn Cys Val
      170                     175                     180
Pro Ile Thr Val Pro His Thr Ser Ser Gln Gly Asn Leu Tyr Glu
      185                     190                     195

```

```
Arg Val Thr Arg Gln Ala Gly Val Thr Pro Asn Lys Val Thr Phe  
          200                      205                210
```

Val Glu

GCACGACGGG	CAAGCCCAAG	GGGGGCGATG	AACAGCCATC	GAGGAATTTG	50
CAATCGCTTA	CTGTGGATGC	AAGATGCTTA	CAAACATACT	GAAACTGATC	100
GCGTTCTGCA	AAAAACGCCT	TTTAGTTTCG	ACGTTTCCGT	TTGGGAGTTT	150
TTCTGGCCTC	TCTTGACAGG	GGCGCGTTTA	GTGATGGCTC	AACCAGGCGG	200
ACAGCGAGAT	GCAACTTACT	TAATTAACAC	CATCGTCCAA	GAGGAAATTA	250
CAACACTGCA	TTTTGTCCCC	TCCATGTTGC	GGATATTTCT	CCAAACTAAA	300
GGGCTAGAAC	GTTGTCAATC	TCTAAAACGG	GTGTTTTGTA	GTGGAGAAGC	350
CTTACCAGTT	GACCTCCAGG	AGCGGTTTTT	TGACTCGATG	GGATGTGAAC	400
TACACAACCT	CTATGGTCCT	ACCGAAGCGG	CAATTGATGT	CACATTTTGG	450
CAGTGTCAAA	GAGAGAGTAA	CTTAAAAGT	GTACCGATTG	GGAGAGCCAT	500
CGCCAACACT	CAAMTTTATA	TCTTCGACTC	CCATTTACAA	GCAGTTCCTT	550
TGGGTGCGAT	CGGCGAACTT	TATATTGGTG	GTATCGGCGT	TGCTAGAGGS	600
TATCTTAACC	GTCCAGACTT	AACAGCCGAG	CGATTTATTT	CCCATCCCTT	650
TAAGGAAGGC	GRRAAACTTT	ACAAAACAGG	AGACTTAGCC	CGATATCTGG	700
CCGATGGCAA	TATCGAATAC	ATCGGTAGAA	TTGATCATCA	AGTAAAAATT	750
CGGGGTTTCC	GCATCGAACT	TGGAGAAATC	GAAACTTTAC	TAGCACAACA	800
CCCGACCATA	CAGCAAACTG	TCGTACACAGC	TAGAATTGAT	CATCTCGAAA	850
ACCAGCGATT	AGTCGCCTAC	ATCGTTCCCTC	ATTCAGAGCA	GACACTAACC	900
ACAGACGAAC	TGCGCCACTT	CCTCAAAAAG	AAACTGCCAG	AATATATGGT	950
GCCTAGTACT	TTCGTTTTTC	TAGACACTCT	ACCCCTAACC	CCCAACGGCA	1000
AAATTGACCG	TCGCGCTTTA	CCAGCACCCG	ACTCAACAAG	GCTTGATTCA	1050
GAAACACAT	ATCTTGCTCC	CCGCGATTAA	TTAGAATTTT	AGTTGACTAA	1100
AATTTGGTCA	GAAATTTTAG	GTATCCAGCC	TATCGGTGTC	AGGGACAAC	1150
TCTTCTTCCT	TGGGCGGCC	CTCCCTT			1177

Ala Arg Arg Ala Ser Pro Arg Gly Ala Met Asn Ser His Arg Gly
5 10 15

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Ile	Cys	Asn	Arg	Leu	Leu	Trp	Met	Gln	Asp	Ala	Tyr	Lys	Leu	Thr	20	25	30
Glu	Thr	Asp	Arg	Val	Leu	Gln	Lys	Thr	Pro	Phe	Ser	Phe	Asp	Val	35	40	45
Ser	Val	Trp	Glu	Phe	Phe	Trp	Pro	Leu	Leu	Thr	Gly	Ala	Arg	Leu	50	55	60
Val	Met	Ala	Gln	Pro	Gly	Gly	Gln	Arg	Asp	Ala	Thr	Tyr	Leu	Ile	65	70	75
Asn	Thr	Ile	Val	Gln	Glu	Glu	Ile	Thr	Thr	Leu	His	Phe	Val	Pro	80	85	90
Ser	Met	Leu	Arg	Ile	Phe	Leu	Gln	Thr	Lys	Gly	Leu	Glu	Arg	Cys	95	100	105
Gln	Ser	Leu	Lys	Arg	Val	Phe	Cys	Ser	Gly	Glu	Ala	Leu	Pro	Val	110	115	120
Asp	Leu	Gln	Glu	Arg	Phe	Phe	Asp	Ser	Met	Gly	Cys	Glu	Leu	His	125	130	135
Asn	Leu	Tyr	Gly	Pro	Thr	Glu	Ala	Ala	Ile	Asp	Val	Thr	Phe	Trp	140	145	150
Gln	Cys	Gln	Arg	Glu	Ser	Asn	Leu	Lys	Ser	Val	Pro	Ile	Gly	Arg	155	160	165
Ala	Ile	Ala	Asn	Thr	Gln	Xaa	Tyr	Ile	Leu	Asp	Ser	His	Leu	Gln	170	175	180
Ala	Val	Pro	Leu	Gly	Ala	Ile	Gly	Glu	Leu	Tyr	Ile	Gly	Gly	Ile	185	190	195
Gly	Val	Ala	Arg	Gly	Tyr	Leu	Asn	Arg	Pro	Asp	Leu	Thr	Ala	Glu	200	205	210
Arg	Phe	Ile	Ser	His	Pro	Phe	Lys	Glu	Gly	Gly	Lys	Leu	Tyr	Lys	215	220	225
Thr	Gly	Asp	Leu	Ala	Arg	Tyr	Leu	Ala	Asp	Gly	Asn	Ile	Glu	Tyr	230	235	240
Ile	Gly	Arg	Ile	Asp	His	Gln	Val	Lys	Ile	Arg	Gly	Phe	Arg	Ile	245	250	255
Glu	Leu	Gly	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Gln	His	Pro	Thr	Ile	260	265	270
Gln	Gln	Thr	Val	Val	Thr	Ala	Arg	Ile	Asp	His	Leu	Glu	Asn	Gln	275	280	285
Arg	Leu	Val	Ala	Tyr	Ile	Val	Pro	His	Ser	Glu	Gln	Thr	Leu	Thr			

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290		295	300
Thr Asp Glu Leu Arg	His Phe Leu Lys	Lys Lys Leu Pro Glu Tyr	
305		310	315
Met Val Pro Ser Thr	Phe Val Phe Leu Asp	Thr Leu Pro Leu Thr	
320		325	330
Pro Asn Gly Lys Ile	Asp Arg Arg Ala Leu	Pro Ala Pro Asp Ser	
335		340	345
Thr Arg Leu Asp Ser	Glu Asn Thr Tyr Leu	Ala Pro Arg Asp Xaa	
350		355	360
Leu Glu Phe Gln Leu	Thr Lys Ile Trp Ser	Glu Ile Leu Gly Ile	
365		370	375
Gln Pro Ile Gly Val	Arg Asp Asn Phe Phe	Phe Leu Gly Arg Pro	
380		385	390

Leu Pro

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ser Ile Arg Thr	Val Val Thr Gly	Leu Gly Ile Ala Ala Pro	
5		10	15
Asn Gly Leu Gly Ile	Glu Glu Tyr Trp Ser	Ala Thr Leu Ala Gly	
20		25	30
Arg Gly Ala Ile Gly	Pro Leu Thr Arg Phe	Asp Ala Ser Ser Tyr	
35		40	45
Pro Ser Arg Leu Ala	Gly Glu Ile Arg Gly	Phe Thr Ala Ala Glu	
50		55	60
His Leu Pro Gly Arg	Leu Leu Pro Gln Thr	Asp Arg Met Thr Gln	
65		70	75
Leu Ala Leu Val Ser	Ala Gly Trp Ala Leu	Asp Asp Ala Gly Val	
80		85	90
Val Pro Asp Glu Leu	Pro Ala Tyr Asp Met	Gly Val Ile Thr Ala	
95		100	105

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Ser	His	Ala	Gly	Gly	Phe	Glu	Phe	Gly	Gln	Asn	Glu	Leu	Lys	Ala
				110					115					120
Leu	Trp	Ser	Lys	Gly	Gly	Lys	Tyr	Val	Ser	Ala	Tyr	Gln	Ser	Phe
				125					130					135
Ala	Trp	Phe	Tyr	Ala	Val	Asn	Ser	Gly	Gln	Ile	Ser	Ile	Arg	Asn
				140					145					150
Gly	Met	Arg	Gly	Pro	Ser	Gly	Val	Val	Val	Ser	Asp	Gln	Ala	Gly
				155					160					165
Gly	Leu	Asp	Ala	Leu	Ala	Gln	Ala	Arg	Arg	Gln	Ile	Arg	Lys	Gly
				170					175					180
Thr	Pro	Leu	Ile	Val	Ser	Gly	Ala	Val	Asp	Ala	Ser	Leu	Cys	Thr
				185					190					195
Trp	Gly	Trp	Val	Ala	Gln	Leu	Ala	Gly	Gly	Arg	Leu	Ser	Arg	Ser
				200					205					210
Asp	Asp	Pro	Gly	His	Ala	Tyr	Val	Pro	Phe	Asp	Asp	Ala	Ala	Val
				215					220					225
Gly	His	Val	Pro	Gly	Glu	Gly	Gly	Ala	Leu	Leu	Ile	Leu	Glu	Glu
				230					235					240
Ala	Glu	His	Ala	Arg	Ser	Arg	Gly	Ala	Arg	Arg	Ile	Tyr	Gly	Glu
				245					250					255
Ile	Thr	Gly	His	Ala	Ser	Thr	Phe	Asp	Pro	Pro	Pro	Trp	Ser	Gly
				260					265					270
Arg	Gly	Pro	Ala	Val	Gln	Arg	Val	Ile	Glu	Glu	Ala	Leu	Ala	Asp
				275					280					285
Ala	Gly	Thr	Val	Pro	Asp	Glu	Val	Asp	Val	Val	Phe	Ala	Asp	Ala
				290					295					300
Ala	Ala	Leu	Pro	Glu	Leu	Asp	Arg	Ile	Glu	Ala	Ala	Ala	Ile	Thr
				305					310					315
Lys	Val	Phe	Gly	Pro	His	Ala	Val	Pro	Val	Thr	Ala	Pro	Lys	Thr
				320					325					330
Met	Thr	Gly	Arg	Leu	Tyr	Ser	Gly	Ala	Ala	Pro	Leu	Asp	Val	Ala
				335					340					345
Ala	Ala	Cys	Leu	Ala	Ile	Arg	Asp	Gly	Leu	Ile	Pro	Pro	Thr	Ile
				350					355					360
His	Ser	Ser	Leu	Ser	Gly	Arg	Tyr	Glu	Ile	Asp	Leu	Val	Thr	Gly
				365					370					375
Ala	Pro	Arg	Thr	Ala	Pro	Val	Arg	Thr	Ala	Leu	Val	Val	Ala	Arg

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	380		385		390
Gly His Gly Gly Phe Asn Ser Ala Val Val Val Arg Ala Pro Arg					
	395		400		405

Asp

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Thr Ser Glu Leu Leu Glu Arg Thr Ala Val Arg Ser Ala Thr			
	5	10	15
Ala Val Phe Thr Gly Ile Gly Val Thr Ala Pro Asn Gly Leu Gly			
	20	25	30
Thr Ala Ala Trp Trp Gln Ala Thr Val Ala Gly Glu Ser Gly Ile			
	35	40	45
Arg Pro Val Ser Arg Phe Asp Ala Ser Gly Tyr Pro Ser Thr Leu			
	50	55	60
Ala Gly Glu Val Pro Gly Phe Asp Ala Glu Glu His Ile Pro Ser			
	65	70	75
Arg Leu Leu Ser Gln Thr Asp His Met Thr Arg Leu Ala Leu Thr			
	80	85	90
Ala Ala Lys Glu Ala Leu Glu Asp Ser Gly Ala Asp Pro Ala Glu			
	95	100	105
Met Pro Gln Tyr Ser Ala Gly Ala Val Thr Ala Ala Ser Ala Gly			
	110	115	120
Gly Phe Glu Phe Gly Gln Arg Glu Leu Gln Ala Leu Trp Ser Lys			
	125	130	135
Gly Gly Gln Tyr Val Ser Ala Tyr Gln Ser Tyr Ala Trp Phe Tyr			
	140	145	150
Ala Val Asn Thr Gly Gln Ile Ser Ile Arg His Gly Leu Arg Gly			
	155	160	165
Pro Ser Gly Val Leu Val Thr Glu Gln Ala Gly Gly Leu Glu Ala			
	170	175	180

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Val	Ala	Gln	Ala	Arg	Arg	Gln	Leu	Arg	Lys	Gly	Ser	Lys	Leu	Ile	185	190	195
Val	Thr	Gly	Gly	Val	Asp	Gly	Ala	Val	Cys	Pro	Trp	Gly	Trp	Thr	200	205	210
Ala	Gln	Leu	Ala	Gly	Gly	Arg	Met	Ser	Pro	Val	Ala	Asp	Pro	Ala	215	220	225
Arg	Ala	Phe	Leu	Pro	Phe	Asp	Ser	Glu	Ala	Ser	Gly	Tyr	Val	Ala	230	235	240
Gly	Glu	Gly	Gly	Ala	Ile	Leu	Val	Leu	Glu	Asp	Ala	Glu	Ala	Ala	245	250	255
Arg	Glu	Arg	Gly	Ala	Arg	Ile	Tyr	Gly	Arg	Leu	Ser	Gly	Tyr	Ala	260	265	270
Ala	Thr	Phe	Asp	Pro	Ala	Pro	Gly	Arg	Gly	Gly	Glu	Pro	Gly	Leu	275	280	285
Arg	Arg	Ala	Ala	Glu	Leu	Ala	Leu	Thr	Glu	Ala	Gly	Leu	Ser	Ala	290	295	300
Ser	Asp	Val	Asp	Val	Val	Phe	Ala	Asp	Ala	Ser	Gly	Val	Pro	Glu	305	310	315
Leu	Asp	Arg	Gln	Glu	Glu	Ala	Ala	Leu	Thr	Ala	Leu	Phe	Gly	Pro	320	325	330
Arg	Gly	Val	Pro	Val	Thr	Ala	Pro	Lys	Thr	Met	Thr	Gly	Arg	Leu	335	340	345
Ser	Ala	Gly	Gly	Ala	Ser	Leu	Asp	Leu	Ala	Ala	Ala	Leu	Leu	Ser	350	355	360
Ile	Arg	Asp	Ala	Val	Ile	Pro	Pro	Thr	Val	Asn	Val	Thr	Ser	Pro	365	370	375
Val	Ala	Ala	Asp	Ala	Leu	Asp	Leu	Val	Thr	Glu	Ala	Arg	Arg	Gly	380	385	390
Pro	Val	Arg	Thr	Ala	Leu	Val	Leu	Ala	Arg	Gly	Thr	Gly	Gly	Phe	395	400	405
Asn	Ala	Ala	Ala	Val	Val	Thr	Ala	Ala	Asn						410	415	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

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(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ile	Pro	Val	Ala	Val	Thr	Gly	Met	Gly	Val	Ala	Ala	Pro	Asn	5	10	15
Gly	Leu	Gly	Ala	Ala	Asp	Tyr	Trp	Ala	Ala	Thr	Arg	Gly	Gly	Lys	20	25	30
Ser	Gly	Ile	Gly	Arg	Ile	Thr	Arg	Phe	Asp	Pro	Ser	Ser	Tyr	Pro	35	40	45
Ala	Arg	Leu	Ala	Gly	Glu	Ile	Pro	Gly	Phe	Glu	Ala	Ala	Glu	His	50	55	60
Leu	Pro	Gly	Arg	Leu	Leu	Pro	Gln	Thr	Asp	Arg	Val	Thr	Arg	Leu	65	70	75
Ser	Leu	Ala	Ala	Ala	Asp	Trp	Ala	Leu	Ala	Asp	Ala	Gly	Val	Glu	80	85	90
Pro	Glu	Ser	Phe	Asp	Pro	Leu	Asp	Met	Gly	Val	Val	Thr	Ala	Gly	95	100	105
His	Ala	Gly	Gly	Phe	Glu	Phe	Gly	Gln	Gly	Glu	Leu	Gln	Lys	Leu	110	115	120
Trp	Ala	Lys	Gly	Ser	Gln	Phe	Val	Ser	Ala	Tyr	Gln	Ser	Phe	Ala	125	130	135
Trp	Phe	Tyr	Ala	Val	Asn	Ser	Gly	Gln	Ile	Ser	Ile	Arg	His	Gly	140	145	150
Met	Lys	Gly	Pro	Asn	Gly	Val	Val	Val	Ser	Asp	Gln	Ala	Gly	Gly	155	160	165
Leu	Asp	Ala	Leu	Ala	Gln	Ala	Arg	Arg	Leu	Val	Arg	Lys	Gly	Thr	170	175	180
Pro	Leu	Ile	Val	Cys	Gly	Ala	Val	Asp	Ala	Ser	Ile	Cys	Pro	Trp	185	190	195
Gly	Trp	Val	Ala	Gln	Leu	Ala	Gly	Gly	Arg	Met	Ser	Asp	Ser	Asp	200	205	210
Glu	Pro	Ala	Arg	Ala	Tyr	Leu	Pro	Phe	Asp	Arg	Asp	Ala	Arg	Gly	215	220	225
Tyr	Leu	Pro	Gly	Glu	Gly	Gly	Ala	Ile	Leu	Ile	Met	Glu	Pro	Ala	230	235	240
Ala	Ala	Ala	Arg	Ala	Arg	Gly	Ala	Lys	Val	Tyr	Gly	Glu	Ile	Ser	245	250	255
Gly	Tyr	Gly	Ala	Thr	Phe	Asp	Pro	Pro	Pro	Gly	Ser	Gly	Ser	Gly			

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	260		265		270
Ser Thr Leu Arg	Thr Ala Ile Arg Val	Ala Leu Asp Asp Ala Gly			
	275	280			285
Val Ala Pro Gly	Asp Val Asp Ala Val	Phe Ala Asp Gly Ala Gly			
	290	295			300
Val Pro Glu Leu	Asp Arg Ala Glu Ala	Glu Ala Ile Thr Asp Val			
	305	310			315
Phe Gly Ser Gly	Gly Val Pro Val Thr	Val Pro Lys Thr Met Thr			
	320	325			330
Gly Arg Leu Tyr	Ser Gly Ala Ala Pro	Leu Asp Val Ala Cys Ala			
	335	340			345
Leu Leu Ala Met	Gln Ala Gly Val Ile	Pro Pro Thr Val His Ile			
	350	355			360
Asp Pro Cys Pro	Glu Tyr Gly Leu Asp	Leu Val Leu His Gln Ala			
	365	370			375
Arg Pro Ala Thr	Val Arg Thr Ala Leu	Val Leu Ala Arg Gly His			
	380	385			390
Gly Gly Phe Asn	Ser Ala Met Ala Val	Arg Ala Gly Arg			
	395	400			

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

Met Ser Ala Arg	Phe Leu Val Thr Gly	Ile Gly Val Ala Ala Pro
	5	10
Ser Gly Leu Gly	Val Glu Asp Phe Trp	Ser Val Thr Arg Ile Gly
	20	25
Lys Asn Ala Ile	Gly Pro Val Thr Arg	Phe Asp Ala Ser Ala Tyr
	35	40
Pro Ser Arg Leu	Ala Gly Glu Ile His	Gly Phe Glu Pro Lys Glu
	50	55
His Leu Pro Gly	Arg Leu Val Pro Gln Thr	Asp Arg Val Thr Gln
	65	70

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Leu	Ala	Leu	Val	Ala	Ala	Asp	Cys	Ala	Phe	Ala	Asp	Ala	Gly	Ile	
				80					85					90	
Glu	Pro	Gly	Thr	Ile	Asp	Pro	Tyr	Ala	Met	Gly	Val	Val	Thr	Ala	
				95					100					105	
Ala	Gly	Ala	Gly	Gly	Phe	Glu	Phe	Ala	Glu	Asn	Glu	Leu	Arg	Lys	
				110					115					120	
Leu	Trp	Ser	Glu	Gly	Ala	Lys	Arg	Val	Ser	Ala	Tyr	Gln	Ser	Phe	
				125					130					135	
Ala	Trp	Phe	Tyr	Ala	Val	Asn	Ser	Gly	Gln	Ile	Ser	Ile	Arg	Asn	
				140					145					150	
Gly	Leu	Arg	Gly	Pro	Ala	Gly	Val	Val	Ile	Ser	Asp	Gln	Ala	Gly	
				155					160					165	
Gly	Leu	Asp	Ala	Leu	Ala	Gln	Ala	Arg	Arg	Gln	Leu	Arg	Lys	Gly	
				170					175					180	
Ser	Lys	Leu	Ile	Ala	Thr	Gly	Gly	Phe	Asp	Ala	Pro	Ile	Cys	Ser	
				185					190					195	
Leu	Gly	Trp	Ala	Ser	Gln	Pro	Arg	Thr	Gly	Gly	Leu	Met	Phe	His	
				200					205					210	
Glu	Arg	Thr	Glu	Pro	Glu	Arg	Ala	Tyr	Leu	Pro	Phe	Glu	Asp	Ala	
				215					220					225	
Ala	Ala	Gly	Tyr	Val	Pro	Gly	Glu	Gly	Gly	Ala	Met	Leu	Ile	Leu	
				230					235					240	
Glu	Asp	Glu	Asp	Ser	Ala	Arg	Asp	Arg	Gly	Ala	Arg	Thr	Val	Tyr	
				245					250					255	
Gly	Glu	Phe	Ala	Gly	Tyr	Gly	Ala	Thr	Leu	Asp	Pro	Lys	Pro	Gly	
				260					265					270	
Ser	Gly	Arg	Glu	Pro	Gly	Leu	Arg	Arg	Ala	Ile	Asp	Val	Ala	Leu	
				275					280					285	
Thr	Asp	Ala	Ala	Cys	His	Pro	Ala	Glu	Val	Glu	Val	Val	Phe	Ala	
				290					295					300	
Asp	Gly	Ala	Ala	Thr	Pro	Arg	Leu	Asp	Arg	Glu	Glu	Ala	Glu	Ala	
				305					310					315	
Ile	Thr	Ala	Val	Phe	Gly	Pro	Arg	Ala	Val	Pro	Val	Thr	Val	Pro	
				320					325					330	
Lys	Thr	Met	Thr	Gly	Arg	Ile	Asn	Ser	Gly	Gly	Ala	Pro	Ile	Asp	
				335					340					345	
Val	Val	Ser	Ala	Val	Leu	Ser	Met	Arg	Glu	Gly	Leu	Ile	Pro	Pro	

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	350		355		360
Thr Thr Asn Val	Glu Leu Ser Asp Ala	Tyr Asp Leu Asp Leu	Val		
	365	370		375	
Ala Val Arg Pro	Arg Thr Ala Ser Val	Arg Thr Ala Leu Val	Leu		
	380	385		390	
Ala Arg Gly Arg	Gly Gly Phe Asn Ser	Ala Val Val Val Arg	Ala		
	395	400		405	

Val Asp

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGATCTGCTT	GAGGTAGTCT	ACGAGGCACT	GGAGTCAGCA	GGGTACTTTG	50
GCGCCAAGTC	AAACCCGGAA	CCTGATGACT	ATGGATGCTA	TATCGGTGCA	100
GTGATGAACA	ACTACTATGA	CAACGTTTCT	TGCCATCCAC	CCACCGCATA	150
CGCTACTCTT	GGAACGTCGC	GTTGCTTCCT	TAGTGGCTGC	ATGAGCCATT	200
ACTTTGGATG	GACGGGACCT	TCCTTGACCA	TTGATACGGC	TTGCTCGTCA	250
TCACTAGTTG	CTATAAACAC	CGCTTGTTAGA	GCAATATGGT	CTGGTGAGTG	300
CTCCCGGGCC	ATAGCTGGGG	GTACCAATGT	CTTCACAAGT	CCGTTTGACT	350
ACCAGAATCT	TCGCGCCGCA	GGATTCCTCA	GCCCTAGCGG	GCAATGCAAG	400
CCGTTTGATG	CTTCTGCTGA	TGGCTACTGC	CGTGGAGAAG	GAGTTGGTGT	450
CGTTGTGCTT	AAGCCTTTGA	CGGCTGCTAT	GCAAGAGAAC	GATAACATCC	500
TTGGCGTCAT	TGTGGGGTCT	GCAGCAAACC	AAAACCAAAA	CCTCAGTCAT	550
ATCACGGTGC	CCCATTCGGG	CTCACAAGTC	CAGCTTTATC	GAAAGGTGAT	600
GAAGCTTGCA	GGTATAGAGC	CAGAGTCAGT	CTCCTACGTT	GAG	643

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ile Leu Leu Gln Val Ala Tyr Glu Ala Leu Glu Met Ser Gly Tyr		
	5	10
		15
Phe Ala Asp Ser Ser Arg Pro Glu Asp Val Gly Cys Tyr Ile Gly		
	20	25
		30
Ala Cys Ala Thr Asp Tyr Asp Phe Asn Val Ala Ser His Pro Pro		

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	35		40		45
Thr Ala Tyr Ser	Ala Thr Gly Thr Leu Arg	Ser Phe Leu Ser Gly			
	50	55			60
Lys Leu Ser His	Tyr Phe Gly Trp Ser Gly	Pro Ser Leu Val Leu			
	65	70			75
Asp Thr Ala Cys	Ser Ser Ser Ala Val Ala	Ile His Thr Ala Cys			
	80	85			90
Thr Ala Leu Arg	Thr Gly Gln Cys Ser Gln	Ala Leu Ala Gly Gly			
	95	100			105
Ile Thr Leu Met	Thr Ser Pro Tyr Leu Tyr	Glu Asn Phe Ser Ala			
	110	115			120
Ala His Phe Leu	Ser Pro Thr Gly Gly Ser	Lys Pro Phe Ser Ala			
	125	130			135
Xaa Ala Asp Gly	Tyr Cys Arg Gly Glu Gly	Gly Gly Leu Val Val			
	140	145			150
Leu Lys Arg Leu	Ser Asp Ala Leu Arg Asp	Asp Asp His Ile Ile			
	155	160			165
Ser Val Ile Ala	Gly Ser Ala Val Asn Gln	Asn Asp Asn Cys Val			
	170	175			180
Pro Ile Thr Val	Pro His Thr Ser Ser Gln	Gly Asn Leu Tyr Glu			
	185	190			195
Arg Val Thr Arg	Gln Ala Gly Val Thr Pro	Asn Lys Val Thr Phe			
	200	205			210

Val Glu

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AATCCTCATG	GAATCAGCTT	GGCAAACACT	AGAAAACGCT	GGCATAACTG	50
CGAACAAAGT	AGCTGGCAGC	AGTACAGGAG	TTTTTGTGGG	TGCTAGTGGC	100
TCTGATTACT	GTTGGGTAAT	GGAGCGGGTA	GGTATTCCCA	TAGAAGCTCA	150
CGTTGCAACG	GGCACGTCGT	TGGCAGCGCT	GGCAAATCGC	ATCTCTTACT	200
TTTTTGACTT	GCGAGGCCCA	AGCATCGTCA	TTGATACGGC	GTGTTCTAGT	250
TCGTTGATGG	CAGTGCATCA	GGCGGTTCAA	TCTATCCGAG	CAGGTGAGTG	300

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CTTACAAGCA	CTGGTGGGCG	GTATACATAT	CATGAGCCAT	CCGGCTAACA	350
GTATTGCATA	TTACAAGGCT	GGGATGTTGG	CGCATGATGG	CAAGTGCAAG	400
ACATTTGACG	ATCGCGCAGA	TGGGTACGTT	CGCAGTGAAG	GCGCTGTGAT	450
GCTTCTGCTC	AAGCAATTGC	ATCAGGCGGA	AGCAGATGGC	GATCTAATTT	500
ATGCGACAAT	CAAGGGGTCA	GCCTCGAATC	ATGGTGGGCA	GTCCGCCGGC	550
CTCACCGTAC	CGAATCCGCA	ACAGCAGGCA	GCACCTTTAA	CCAATGCCTG	600
GAAAGCCTCT	GGTGTGAGAC	CTAACACGAT	TAGTTTTATC	GAA	643

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

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(v) FRAGMENT TYPE: internal fragment
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Leu Met Glu Ser Ala Trp Gln Thr Leu Glu Asn Ala Gly Ile
5 10 15

Thr Ala Asn Lys Val Ala Gly Ser Ser Thr Gly Val Phe Val Gly
20 25 30

Ala Ser Gly Ser Asp Tyr Cys Trp Val Met Glu Arg Val Gly Ile
35 40 45

Pro Ile Glu Ala His Val Ala Thr Gly Thr Ser Leu Ala Ala Leu
40 55 60

Ala Asn Arg Ile Ser Tyr Phe Phe Asp Leu Arg Gly Pro Ser Ile
65 70 75

Val Ile Asp Thr Ala Cys Ser Ser Ser Leu Met Ala Val His Gln
80 85 90

Ala Val Gln Ser Ile Arg Ala Gly Glu Cys Leu Gln Ala Leu Val
95 100 105

Gly Gly Ile His Ile Met Ser His Pro Ala Asn Ser Ile Ala Tyr
110 115 120

Tyr Lys Ala Gly Met Leu Ala His Asp Gly Lys Cys Lys Thr Phe
125 130 135

Asp Asp Arg Ala Asp Gly Tyr Val Arg Ser Glu Gly Ala Val Met
140 145 150

Leu Leu Leu Lys Gln Leu His Gln Ala Glu Ala Asp Gly Asp Leu
155 160 165

Ile Tyr Ala Thr Ile Lys Gly Ser Ala Ser Asn His Gly Gly Gln
170 175 180

[illegible]

TATATTACTC	CAGGTTGCTT	ACGAAGCATT	GGAAATGTCC	GGGTATTTTCG	50
CCGACTCGTC	CAAGCCTGAG	GACGTAGGTT	GCTATATTGG	AGCTTGTGCA	100
ACAGATTACG	ATTTTCAGCGT	AGCGTCCCAT	CCTCCTACGG	CATACTCAGC	150
AACTGGCACG	CTCCGATCTT	TCCTGAGTGG	CAAGCTGTCA	CATTACTTTG	200
GTTGGTCTGG	TCCCTCTCTT	GTCCTGGACA	CCGCCTGCTC	TTCATCGGCG	250
GTGGCCATTC	ACACTGCATG	TACTGCTTTG	AGGACTGGCC	AGTGTTCTCA	300
GGCTTTAGCA	GGCGGGGATTA	CTTTGATGAC	CAGCCCGTAT	CTCTTTGAGA	350
ACTTTGCTGC	CGCCCATTTC	TTGAGCCCAA	CGGGAGGCTC	AAAGCCGTTT	400
AGTGCGAGATG	CAGATGGGTA	TTGTAGAGGA	GAAGGGGGTG	GGCTCGTGTT	450
CTTGAAACGA	CTTTCAGATG	CTATCAGGA	TAACGACCAC	ATCATTAGCG	500
TCATCGTCTGG	CTCAGCCGTC	AACCAGAAAG	CTAACTGTGT	GCCTATCACC	550
GTCCCTCATA	CTTCGTCTCA	GGGCAATCTC	TATGAACGAG	TTACCGCACA	600
GGCAGGGGTG	ACACCTAATA	AGGTCACCTT	TGTGGAA		637

Ile Leu Leu Gln Val Ala Tyr Glu Ala Leu Glu Met Ser Gly Tyr
5 10 15

Phe Ala Asp Ser Ser Lys Pro Glu Asp Val Gly Cys Tyr Ile Gly
20 25 30

Ala Cys Ala Thr Asp Tyr Asp Phe Ser Val Ala Ser His Pro Pro
35 40 45

Thr Ala Tyr Ser Ala Thr Gly Thr Leu Arg Ser Phe Leu Ser Gly
50 55 60

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Lys	Leu	Ser	His	Tyr	Phe	Gly	Trp	Ser	Gly	Pro	Ser	Leu	Val	Leu
				65					70					75
Asp	Thr	Ala	Cys	Ser	Ser	Ser	Ala	Val	Ala	Ile	His	Thr	Ala	Cys
				80					85					90
Thr	Ala	Leu	Arg	Thr	Gly	Gln	Cys	Ser	Gln	Ala	Leu	Ala	Gly	Gly
				95					100					105
Ile	Thr	Leu	Met	Thr	Ser	Pro	Tyr	Leu	Phe	Glu	Asn	Phe	Ala	Ala
				110					115					120
Ala	His	Phe	Leu	Ser	Pro	Thr	Gly	Gly	Ser	Lys	Pro	Phe	Ser	Ala
				125					130					135
Asp	Ala	Asp	Gly	Tyr	Cys	Arg	Gly	Glu	Gly	Gly	Gly	Leu	Val	Val
				140					145					150
Leu	Lys	Arg	Leu	Ser	Asp	Ala	Ile	Arg	Asp	Asn	Asp	His	Ile	Ile
				155					160					165
Ser	Val	Ile	Ala	Gly	Ser	Ala	Val	Asn	Gln	Asn	Ala	Asn	Cys	Val
				170					175					180
Pro	Ile	Thr	Val	Pro	His	Thr	Ser	Ser	Gln	Gly	Asn	Leu	Tyr	Glu
				185					190					195
Arg	Val	Thr	Ala	Gln	Ala	Gly	Val	Thr	Pro	Asn	Lys	Val	Thr	Phe
				200					205					210

Val Glu

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCATCTGCTA	GAAATCAGCT	ACGAGGCGCT	CGAGAATGCA	GGCTTTCCAC	50
TGCCTAGCAT	TGCTGGCACG	AACATGGGTG	TCTTTGTCCG	CGGAAGCAAC	100
TCTGAGTATC	GAGCGCACAT	CGGAAACGAT	ACCGACAAC	TACCGATGTT	150
TGAAGCAACA	GGCAATGCAG	AATCTCTGCT	GGCGAATCGA	GTCTCTTATG	200
TGTATGATCT	CCACGGCGCA	AGTCTGACGA	TTGGTACCGC	TTGTTCCGTC	250
GAGTTTAGCA	GCTTTGGATA	GCGCGTTTCT	CAGCTTGCAG	CTGGTAAGTC	300
GTCCACAGCA	ATTGTTGCCG	GCTCCGTTGT	TCGAATCGTA	CCGTCATCGA	350
CCATCTCACC	TTCTACTATG	AAGTAAGCAG	TCATGGCTCT	TGACACGGAG	400
ACTACTCACC	ATTCCAGGCT	TCTGTCACCA	GAAGGGCGGT	GTTATGCGTT	450
CGATGACAGA	GCCACTAGTG	GTTTTGGAAG	GGGTGAAGGT	TCTGCCTGCA	500
TAATATTGGA	AACCTTAGAG	GCAGCCTTAA	GAGACAACGA	CCCAATCCGA	550
TCGGTCATTC	GCAATTCGGG	AGTCAATCAA	GATGGTAAAA	CTGCAGGTAT	600

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CACAATGCCA AATGGGGAAG CGCAAGCTTC ATTGATACAA TCTGTTTATC 650
 GCACTGCTGG ATTGGACCCT CTGCAGACAG ATTACGTCGA G 691

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

His	Leu	Leu	Glu	Ile	Ser	Tyr	Glu	Ala	Leu	Glu	Asn	Ala	Gly	Phe	
				5					10					15	
Pro	Leu	Pro	Ser	Ile	Ala	Gly	Thr	Asn	Met	Gly	Val	Phe	Val	Gly	
				20					25					30	
Gly	Ser	Asn	Ser	Glu	Tyr	Arg	Ala	His	Ile	Gly	Asn	Asp	Thr	Asp	
				35					40					45	
Asn	Leu	Pro	Met	Phe	Glu	Ala	Thr	Gly	Asn	Ala	Glu	Ser	Leu	Leu	
				50					55					60	
Ala	Asn	Arg	Val	Ser	Tyr	Val	Tyr	Asp	Leu	His	Gly	Ala	Ser	Leu	
				65					70					75	
Thr	Ile	Gly	Thr	Ala	Cys	Ser	Val	Glu	Phe	Ser	Ser	Phe	Gly	Xaa	
				80					85					90	
Arg	Val	Ser	Gln	Leu	Ala	Ala	Gly	Lys	Ser	Ser	Thr	Ala	Ile	Val	
				95					100					105	
Ala	Gly	Ser	Val	Val	Arg	Ile	Val	Pro	Ser	Ser	Thr	Ile	Ser	Pro	
				110					115					120	
Ser	Thr	Met	Lys	Leu	Leu	Ser	Pro	Glu	Gly	Arg	Cys	Tyr	Ala	Phe	
				125					130					135	
Asp	Asp	Arg	Ala	Thr	Ser	Gly	Phe	Gly	Arg	Gly	Glu	Gly	Ser	Ala	
				140					145					150	
Cys	Ile	Ile	Leu	Glu	Thr	Leu	Glu	Ala	Ala	Leu	Arg	Asp	Asn	Asp	
				155					160					165	
Pro	Ile	Arg	Ser	Val	Ile	Arg	Asn	Ser	Gly	Val	Asn	Gln	Asp	Gly	
				170					175					180	
Lys	Thr	Ala	Gly	Ile	Thr	Met	Pro	Asn	Gly	Glu	Ala	Gln	Ala	Ser	
				185					190					195	
Leu	Ile	Gln	Ser	Val	Tyr	Arg	Thr	Ala	Gly	Leu	Asp	Pro	Leu	Gln	
				200					205					210	

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Thr Asp Tyr Val Glu
215

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:680

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AACTGTTAGA	GGTCAGTTAC	GAGGCGTTTG	AGAATGCGGG	CATATCATT	50
TCGAGTGTTG	CAGGTACCGA	CGTTGGGGTA	TTCATCAGTG	CCAGCACCAA	100
TGATTACCGT	TTCGTTTTCC	ACAACGACCT	CGACACATTG	CCAATGTTTG	150
AATCCACTGG	GAGTGAATTA	TCGATCATGT	CCAATCGTAT	CTCCTATACT	200
TTCAATCTTA	GAGGTCCAAG	TATGACGATT	GATACTCCCT	GTTCTCAAG	250
TTTGATCGCA	CTCCATACAG	CATTCAGAAG	TCTACAGGTC	GGAGAAAGCT	300
CTTGCGCCAT	TGTCGGTGGA	TCTAACCTCC	ACATCACTCC	AGATTCCTAC	350
ATTTCAATTCT	CGACGATGAG	GTAAGCACTA	TCGTTTGCGA	ATTACCTATC	400
TTTGATTACG	AGTGACTAAG	TTGTACAGGC	TCCTGTGCGC	CCATGGACGA	450
TCGTGCAGTC	AATGGGTTTG	GGCGCGGAGA	GGGCACAAGT	TGCATAATAC	500
TGAAGCCTTT	AGATGCCGCA	TTGAAAGACC	ACGATCCCAT	AAGGGCAGTT	550
ATTCGCAATA	CGGGCACTAA	TCAAGATGGG	AAGACGACAG	GTATCACGAT	600
GCCGAATGGT	GAAGCACAGG	CCGCCTTAAT	GCAATCAGTC	TACGAGGCAG	650
CGGGCTTAGA	TCCCCTTGAA	ACAGACTATG			680

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu	Leu	Glu	Val	Ser	Tyr	Glu	Ala	Phe	Glu	Asn	Ala	Gly	Ile	Ser
				5					10					15
Leu	Ser	Ser	Val	Ala	Gly	Thr	Asp	Val	Gly	Val	Phe	Ile	Ser	Ala
				20					25					30
Ser	Thr	Asn	Asp	Tyr	Arg	Phe	Val	Phe	His	Asn	Asp	Leu	Asp	Thr
				35					40					45
Leu	Pro	Met	Phe	Glu	Ser	Thr	Gly	Ser	Glu	Leu	Ser	Ile	Met	Ser
				50					55					60
Asn	Arg	Ile	Ser	Tyr	Thr	Phe	Asn	Leu	Arg	Gly	Pro	Ser	Met	Thr
				65					70					75

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Ile	Asp	Thr	Pro	Cys	Ser	Ser	Ser	Leu	Ile	Ala	Leu	His	Thr	Ala	
				80					85					90	
Phe	Arg	Ser	Leu	Gln	Val	Gly	Glu	Ser	Ser	Cys	Ala	Ile	Val	Gly	
				95					100					105	
Gly	Ser	Asn	Leu	His	Ile	Thr	Pro	Asp	Ser	Tyr	Ile	Ser	Phe	Ser	
				110					115					120	
Thr	Met	Ser	Cys	Thr	Gly	Ser	Cys	Arg	Pro	Met	Asp	Asp	Arg	Ala	
				125					130					135	
Val	Asn	Gly	Phe	Gly	Arg	Gly	Glu	Gly	Thr	Ser	Cys	Ile	Ile	Leu	
				140					145					150	
Lys	Pro	Leu	Asp	Ala	Ala	Leu	Lys	Asp	His	Asp	Pro	Ile	Arg	Ala	
				155					160					165	
Val	Ile	Arg	Asn	Thr	Gly	Thr	Asn	Gln	Asp	Gly	Lys	Thr	Thr	Gly	
				170					175					180	
Ile	Thr	Met	Pro	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Leu	Met	Gln	Ser	
				185					190					195	
Val	Tyr	Glu	Ala	Ala	Gly	Leu	Asp	Pro	Leu	Glu	Thr	Asp	Tyr		
				200					205						

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCATTTGCTG	GAGGTGAGCT	ATGAAGCGCT	TGAAAATGCT	GGCCTTTCTC	50
TTCCTTGCA	TGCCGGCACC	AAAATGGGAG	TCTTCGTTGG	TGGAGGCAAT	100
GCAKAGTATC	GATCGCATAT	CGGCCAAGAT	ATTGACAATC	TGCCTATGTT	150
CGAGGCAACT	GGTAACGCAG	AGGCGCTATT	GGCGAATAGA	GTTTCTTATG	200
TATATGATCT	TCGAGGACCG	AGTCTAACCA	CCGATACCGC	CTGTTCTCTCA	250
AGTCTCGCCG	CTTTGAACAC	GGCATTCTTA	AGTCTACAGG	CTGGCGAGTC	300
GTCTACAGCA	CTGGTCGGTA	GCTCAGTAAT	TCGGCTTAGG	CCTGAGTCAG	350
CCATCTCACT	TTCCAGCATG	CAGTAAGTCC	TTCATGGTGC	ACCTGCATAC	400
ATTGCTAATA	AGTGCAGGCT	TCTATCCCCA	GATGGAAAAT	CTTACGCGTT	450
CGATGAGAGA	GCTACCAAGTG	GTTTTGGAAG	GGGTGAGGGT	TCGGGTTGCA	500
TAATACTAAA	ACCCCTGGAC	GCAGCCGTGA	GAGACGGAGA	CCCAATTAGA	550
GCAGTCATTT	GTAACCTCGG	TGTAAACCAA	GACGGCAAGA	CTGCTGGTAT	600
TACAATGCCT	AATGGACACG	CGCAAGCTTC	TCTAATACGG	TCTGTTTATC	650
AGTCTACAGG	GATAGACCCT	TTAATGACGG	ACTATGTCGA	A	691

(2) INFORMATION FOR SEQ ID NO:40:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His	Leu	Leu	Glu	Val	Ser	Tyr	Glu	Ala	Leu	Glu	Asn	Ala	Gly	Leu	5	10	15
Ser	Leu	Pro	Cys	Ile	Ala	Gly	Thr	Lys	Met	Gly	Val	Phe	Val	Gly	20	25	30
Gly	Gly	Asn	Ala	Xaa	Tyr	Arg	Ser	His	Ile	Gly	Gln	Asp	Ile	Asp	35	40	45
Asn	Leu	Pro	Met	Phe	Glu	Ala	Thr	Gly	Asn	Ala	Glu	Ala	Leu	Leu	50	55	60
Ala	Asn	Arg	Val	Ser	Tyr	Val	Tyr	Asp	Leu	Arg	Gly	Pro	Ser	Leu	65	70	75
Thr	Thr	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Ala	Ala	Leu	Asn	Thr	80	85	90
Ala	Phe	Leu	Ser	Leu	Gln	Ala	Gly	Glu	Ser	Ser	Thr	Ala	Leu	Val	95	100	105
Gly	Ser	Ser	Val	Ile	Arg	Leu	Arg	Pro	Glu	Ser	Ala	Ile	Ser	Leu	110	115	120
Ser	Ser	Met	Gln	Leu	Leu	Ser	Pro	Asp	Gly	Lys	Ser	Tyr	Ala	Phe	125	130	135
Asp	Glu	Arg	Ala	Thr	Ser	Gly	Phe	Gly	Arg	Gly	Glu	Gly	Ser	Gly	140	145	150
Cys	Ile	Ile	Leu	Lys	Pro	Leu	Asp	Ala	Ala	Val	Arg	Asp	Gly	Asp	155	160	165
Pro	Ile	Arg	Ala	Val	Ile	Cys	Asn	Ser	Gly	Val	Asn	Gln	Asp	Gly	170	175	180
Lys	Thr	Ala	Gly	Ile	Thr	Met	Pro	Asn	Gly	His	Ala	Gln	Ala	Ser	185	190	195
Leu	Ile	Arg	Ser	Val	Tyr	Gln	Ser	Thr	Gly	Ile	Asp	Pro	Leu	Met	200	205	210
Thr	Asp	Tyr	Val	Glu											215		

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 637

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GCTGTTTCTT CAAACTAGCT GGCAATGCAT TGAAGATGCG GGATATAACC 50
CCACATCCTT TGCAGGTAGC AAGTGTGGCG TATTTGTCGG CTGCGAAACG 100
GGAGACTATG GAAAGATTGT GCAGCGATAT GAATTGAGCG CTCTCGGATT 150
GCTAGGCTCT TCTGCGGCAC TGCTCCCGGC AAGGATCTCC TATTCCTCA 200
ACCTCCAGGG CCCTTGTATG GCGATCGACA CAGCCTGCTC TGCATCCCTA 250
GTTGCCATAG CCAACGCCTG CGACAGCCTG GTACTGGGTC ACTCCGATGC 300
AGCCTTGGCC GGAGGAGTCT ACGTCCTCTC CGGGCCGGAA ATGCACATTA 350
TGATGAGCAA AGCTGGTATC TTGTCACCCG ATGGCAGATG TTTCACCTTC 400
GATCGACGTG CTAACGGCTT TGTACCGGGC GAAGGTGTGG GCGTCGTGTT 450
ACTCAAACGC CTTGCCGATG CCGAAAAAGA CGGTGATAAT ATCTGTGGTG 500
TGATTCGAGG CTGGGGGGTG AATCAAGACG GCAAGACCAG TGGAATTACA 550
GCACCTAACG GACAGTCACA GCAACGATTG CAGAAAGAAG TCTACGAACG 600
GTTTCAGATT CAGCCAGCAG ACATTCAACT GGTTGAG 637

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Leu Phe Leu Gln Thr Ser Trp Gln Cys Ile Glu Asp Ala Gly Tyr
      5                      10                      15
Asn Pro Thr Ser Phe Ala Gly Ser Lys Cys Gly Val Phe Val Gly
      20                      25                      30
Cys Glu Thr Gly Asp Tyr Gly Lys Ile Val Gln Arg Tyr Glu Leu
      35                      40                      45
Ser Ala Leu Gly Leu Leu Gly Ser Ser Ala Ala Leu Leu Pro Ala
      50                      55                      60
Arg Ile Ser Tyr Phe Leu Asn Leu Gln Gly Pro Cys Met Ala Ile
      65                      70                      75
Asp Thr Ala Cys Ser Ala Ser Leu Val Ala Ile Ala Asn Ala Cys
      80                      85                      90

```

[illegible]

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Met	Ile	Glu	Val	Ala	Tyr	Gln	Gly	Leu	Glu	Ser	Ala	Gly	Leu	5	10	15
Ser	Leu	Gln	Asp	Val	Ala	Gly	Ser	Arg	Thr	Gly	Val	Phe	Ile	Gly	20	25	30
His	Phe	Ser	Ser	Asp	Tyr	Arg	Asp	Met	Ile	Phe	Arg	Asp	Pro	Glu	35	40	45
Arg	Ala	Pro	Thr	Tyr	Thr	Phe	Ser	Gly	Val	Ser	Lys	Thr	Ser	Leu	50	55	60
Ala	Asn	Arg	Ile	Ser	Trp	Leu	Phe	Asp	Leu	Lys	Gly	Pro	Ser	Phe	65	70	75
Ser	Leu	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ala	Leu	His	Leu	80	85	90
Ala	Cys	Gln	Ser	Leu	Arg	Ala	Gly	Glu	Ser	Asp	Ile	Ala	Ile	Val	95	100	105
Gly	Gly	Val	Asn	Leu	Leu	Trp	Asn	Pro	Glu	Leu	Phe	Met	Tyr	Leu	110	115	120
Ser	Asn	Gln	His	Phe	Leu	Ser	Pro	Asp	Gly	Lys	Cys	Lys	Ser	Phe	125	130	135
Asp	Glu	Ser	Gly	Asp	Gly	Tyr	Gly	Arg	Gly	Glu	Gly	Ile	Ala	Ala	140	145	150
Leu	Val	Leu	Arg	Arg	Val	Asp	Asp	Ala	Ile	Ala	Ala	Arg	Asp	Pro	155	160	165
Ile	Arg	Ala	Ile	Ile	Arg	Gly	Thr	Gly	Ser	Asn	Gln	Asp	Gly	His	170	175	180
Thr	Lys	Gly	Phe	Thr	Leu	Pro	Ser	Ala	Glu	Ala	Gln	Ala	Arg	Leu	185	190	195
Ile	Arg	Asp	Thr	Tyr	Ser	Ala	Ala	Gly	Leu	Gly	Phe	Arg	Asp	Thr	200	205	210

Arg Tyr Val Glu

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:655

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

RGTCCTTATG GAGACCGTCT ACGAGGCAAT TGAGTCTGCG GGTATGACTT 50
TGAAGGGGCT GCAAGGCAGC GACACAAGTG TGTATGCCGG CGTCATGTGT 100
GGCGACTACG AGGCCATACA GCTCCGCGAT CTGGACGCGG CCCCAGCTTA 150
TTTCGCAGTG GGAACCTCGC GAGCTATCCT CTCCAATCGA ATCTCGTATT 200
TCTTCAACTG GCACGGCGCG TCCATCACCA TGGACACGGC ATGTTCTCT 250
AGTCTGGTCG CCATTCACTT GGCCGTTTCA RCGCTTCGGG CAAATGAATC 300
ACGRATGGCC GTGGCGTGTG GGTGCAACCT CATTCTCGGA CCCGAGAGTT 350
ACATTATTGA AAGCAAGGTG AAGATGCTGT CCCCAGGACG TCTCAGCCGA 400
ATGTGGGATA AAGACGCCAA CGGCTATGCG CGTGGAGATG GCGTTGCGGC 450
CGTTGTTTTG AAGACTCTCA GCGCCGCGCT GGCGGACGGA GACCACATTG 500
AATGTCTCAT ACGGGAGACG GGAATCAACC AGGACGGTGC GACAGCCGGT 550
CTCACCATGC CTAGCGCCAC TGCAGACGGA GCTCTTATTC ACAGTACGTA 600
CACCAAGGCA GGTCTTGATC TCACTGCCCA GGCAGACCGT CCCAGTATT 650
TCGAG

```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(A) DESCRIPTION: protein
(iii) HYPOTHETICAL: no
(v) FRAGMENT TYPE: internal fragment
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Val Leu Met Glu Thr Val Tyr Glu Ala Ile Glu Ser Ala Gly Met
      5                      10                      15

Thr Leu Lys Gly Leu Gln Gly Ser Asp Thr Ser Val Tyr Ala Gly
      20                      25                      30

Val Met Cys Gly Asp Tyr Glu Ala Ile Gln Leu Arg Asp Leu Asp
      35                      40                      45

Ala Ala Pro Thr Tyr Phe Ala Val Gly Thr Ser Arg Ala Ile Leu
      50                      55                      60

Ser Asn Arg Ile Ser Tyr Phe Phe Asn Trp His Gly Ala Ser Ile
      65                      70                      75

Thr Met Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile His Leu
      80                      85                      90

Ala Val Gln Xaa Leu Arg Ala Asn Glu Ser Arg Met Ala Val Ala
      95                      100                     105

Cys Gly Ser Asn Leu Ile Leu Gly Pro Glu Ser Tyr Ile Ile Glu
      110                     115                     120

Ser Lys Val Lys Met Leu Ser Pro Asp Gly Leu Ser Arg Met Trp

```

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	125		130		135
Asp Lys Asp Ala	Asn Gly Tyr Ala Arg	Gly Asp Gly Val Ala Ala			
	140	145			150
Val Val Leu Lys	Thr Leu Ser Ala Ala	Leu Ala Asp Gly Asp His			
	155	160			165
Ile Glu Cys Leu	Ile Arg Glu Thr Gly	Leu Asn Gln Asp Gly Ala			
	170	175			180
Thr Ala Gly Leu	Thr Met Pro Ser Ala	Thr Ala Gln Arg Ala Leu			
	185	190			195
Ile His Ser Thr	Tyr Thr Lys Ala Gly	Leu Asp Leu Thr Ala Gln			
	200	205			210
Ala Asp Arg Pro	Gln Tyr Phe Glu				
	215				

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

AGGTCTGTTG GAGACGGTTT ATCGCGCCTT TGAAAACGGT AAGGCCACCC 50
TGGGAATAAA CCGGCTTCTC GTCCTGACGG CTTACTCTAT GCTAGCTGGT 100
ATACCCATGG AGCAGGTCCT CGGGTCGAAG ACATCCGTTT ACGTGGGATG 150
TTTCACCCGC GAGTTCGAGC AGTTGCTCGC GAGGGACCCC GAGATGAATC 200
TGAAATACAT CGCTACGGGC ACCGGCACGG CGATGCTGTC GAATCGCCTC 250
TCCTGGTTCT ATGACTTGAA AGGCGCCAGT ATCACTCTTG ATACTGCCTG 300
TTCGTCCAGT CTCAATGCGT GCCATCTTGC TTGCGCAAGC TTACGTAATG 350
GAGAAGCCAA TATGGTAAGA CTCCAACCTCA TCGCGGGACT GAACAATTGC 400
ATACTGATCC ATCAAAGGCC CTGGTAGGAG GCTGCAATCT TTTCTATAAC 450
CCGGAAACGA TCATCCCTCT GACAAATCTA GGCTTTCTTT CTCCGGATAA 500
CAAATGTTAT AGTTTTGACC ATCGTGCTAA CGGTTACTCT CGCGGCGAGG 550
GGTTTGGTAT TCTTGATTG AAGAGACTGT CGGACGCTCT ACGCGATAAC 600
GACACTGTCC GTGCAGTGAT TCGGGCCTCT TCGTCTAACC AGGATGGCAA 650
GTCTCCCGGT ATCACACAGC CTACCAAACA AGCGCAAATA CAACTGATCA 700
AAGACACTTA CGCGGCTGCC GGGCTGGACT ATACGCAAAC CCGCTACTTC 750
GANA
754

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gly	Leu	Leu	Glu	Thr	Val	Tyr	Arg	Ala	Phe	Glu	Asn	Ala	Gly	Ile	5	10	15
Pro	Met	Glu	Gln	Val	Leu	Gly	Ser	Lys	Thr	Ser	Val	Tyr	Val	Gly	20	25	30
Cys	Phe	Thr	Arg	Glu	Phe	Glu	Gln	Leu	Leu	Ala	Arg	Asp	Pro	Glu	35	40	45
Met	Asn	Leu	Lys	Tyr	Ile	Ala	Thr	Gly	Thr	Gly	Thr	Ala	Met	Leu	50	55	60
Ser	Asn	Arg	Leu	Ser	Trp	Phe	Tyr	Asp	Leu	Lys	Gly	Ala	Ser	Ile	65	70	75
Thr	Leu	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Asn	Ala	Cys	His	Leu	80	85	90
Ala	Cys	Ala	Ser	Leu	Arg	Asn	Gly	Glu	Ala	Asn	Met	Ala	Leu	Val	95	100	105
Gly	Gly	Cys	Asn	Leu	Phe	Tyr	Asn	Pro	Glu	Thr	Ile	Ile	Pro	Leu	110	115	120
Thr	Asn	Leu	Gly	Phe	Leu	Ser	Pro	Asp	Asn	Lys	Cys	Tyr	Ser	Phe	125	130	135
Asp	His	Arg	Ala	Asn	Gly	Tyr	Ser	Arg	Gly	Glu	Gly	Phe	Gly	Ile	140	145	150
Leu	Val	Leu	Lys	Arg	Leu	Ser	Asp	Ala	Leu	Arg	Asp	Asn	Asp	Thr	155	160	165
Val	Arg	Ala	Val	Ile	Arg	Ala	Ser	Ser	Ser	Asn	Gln	Asp	Gly	Lys	170	175	180
Ser	Pro	Gly	Ile	Thr	Gln	Pro	Thr	Lys	Gln	Ala	Gln	Ile	Gln	Leu	185	190	195
Ile	Lys	Asp	Thr	Tyr	Ala	Ala	Ala	Gly	Leu	Asp	Tyr	Thr	Gln	Thr	200	205	210
Arg	Tyr	Phe	Xaa														

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:722

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

CTTGTTACTC GAGACTGTCT ACGAATCTCT CGAGTCGGCT GGTCAGACAA 50
TCGAAGGCTT GCAAGGATCG CAAACCGCAG TGTATATTGG TGTAATGTGC 100
GATGATTACG CCGAGCTCGT GTATCATGAT ACAGAGTCAA TCCCGACCTA 150
TGCTGCAACT GGTAGTGCAC GCAGCATGAT GTCGAACCGA ATCTCTTACT 200
TCTTTGACTG GAAGGGGCGG TCAATGACCA TTGATACTGC CTGTTCTCTT 250
AGTCTTGTCG CTGTCCACCA GGCCGTTCAA GTTCTCAGGA GCGGAGAATC 300
CCGCGTCGCA GTGGCTGCTG GGGCAAATCT CATCTTCGGA CCCAGTAAGT 350
CTTCCTAAAA TATGAGTAGG CTCCAGTCAT TGTGATTGCT AATCACTTCA 400
ACCATTTACA GAGATGTACA TTGCTGAGAG CAACCTCAAT ATGTTGTCCC 450
CAACTGGSCG STCCCGAATG TGGGACGCTA ACSCGGATGG CTATGCACGA 500
GGAGAGGGTA TTGCATCTGT CGTACTCAAA ACTCTTAGCT CTGCTATAGC 550
AGATGGTGAT ACCATCGAAT GTTTGATCCG AGAAACCGGT GTCAACCAGG 600
ATGGCCGCAC CACTGGTATC ACTATGCCAA GCTCCGCAGC CCAAGCCAGT 650
TTGATCCGTC AGACTTACGC CAGAGCTGGT TTGGACCTGG CGAAGCAAGC 700
TGATCGGCCT CAATTCTTTG AG                                     722

```

- (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE:
 (A) DESCRIPTION: protein
 (iii) HYPOTHETICAL: no
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Leu Leu Leu Glu Thr Val Tyr Glu Ser Leu Glu Ser Ala Gly Gln
      5                                10                                15

Thr Ile Glu Gly Leu Gln Gly Ser Gln Thr Ala Val Tyr Ile Gly
      20                                25                                30

Val Met Cys Asp Asp Tyr Ala Glu Leu Val Tyr His Asp Thr Glu
      35                                40                                45

Ser Ile Pro Thr Tyr Ala Ala Thr Gly Ser Ala Arg Ser Met Met
      50                                55                                60

Ser Asn Arg Ile Ser Tyr Phe Phe Asp Trp Lys Gly Pro Ser Met
      65                                70                                75

Thr Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln
      80                                85                                90

Ala Val Gln Val Leu Arg Ser Gly Glu Ser Arg Val Ala Val Ala
      95                                100                               105

Ala Gly Ala Asn Leu Ile Phe Gly Pro Lys Met Tyr Ile Ala Glu
      110                               115                               120

```


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Ser	Asn	Leu	Asn	Met	Leu	Ser	Pro	Thr	Gly	Arg	Ser	Arg	Met	Trp
				125					130					135
Asp	Ala	Asn	Xaa	Asp	Gly	Tyr	Ala	Arg	Gly	Glu	Gly	Ile	Ala	Ser
				140					145					150
Val	Val	Leu	Lys	Thr	Leu	Ser	Ser	Ala	Ile	Ala	Asp	Gly	Asp	Thr
				155					160					165
Ile	Glu	Cys	Leu	Ile	Arg	Glu	Thr	Gly	Val	Asn	Gln	Asp	Gly	Arg
				170					175					180
Thr	Thr	Gly	Ile	Thr	Met	Pro	Ser	Ser	Ala	Ala	Gln	Ala	Ser	Leu
				185					190					195
Ile	Arg	Gln	Thr	Tyr	Ala	Arg	Ala	Gly	Leu	Asp	Leu	Ala	Lys	Gln
				200					205					210
Ala	Asp	Arg	Pro	Gln	Phe	Phe	Glu							
				215										

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AATATTACTT	GAGACGATCT	ACGAAGGACT	TGAGTCCGCC	GGA CTTACCA	50
TAAAGGGGCT	GCAAGGTTCC	CAAACAGCTG	TGTACGTCGG	TCTCATGGCT	100
GGAGACTACT	ATGACATCCA	GATGCGCGAC	ATAGAGACTT	TGCCTCGATA	150
TGCTGCTACC	GGGACTGCTC	GTAGCATTAT	GAGCAACCGA	GTCTCTTATT	200
TCTTTGATTG	GAAAGGTCCG	TCCATGACAA	TTGATACGGC	CTGCTCTTCT	250
TCCCTCGTTG	CCGTTTCATCA	GGCTGTGCGAG	ATTCTCCGGA	GAGGTGATGT	300
TACCATGGCT	GTGGCTGCCG	GCGCCAACCT	GATCTATGGT	CCTGAGGCTT	350
ATATATCCGA	GTCGAATCTG	AACATGCTGT	CGCCGAGCGG	AAGATCGCGC	400
ATGTGGGATT	CAAGTGCGGA	CGGATACGGC	CGCGGAGAAG	GGTTTGCGGC	450
AGTGATGTTG	AAGACCCTGA	GCGCTGCAAT	TCGTGATGGA	GATCATATCG	500
AGTGCATTAT	CCGGGAGACA	GGAATTAACC	AGGATGGCAG	AACAGCCGGA	550
ATTACCATGC	CAAGTGCTGT	CAGCCAGACT	CGATTGATCA	AAGACACATA	600
TGCTCGAGCT	GGACTCGATT	GCAGGAAAGA	AGCGGAGAGA	TGCCAGTACT	650
TTGAAGGTAA	GCGAATAACT	TTTCTTGATA	AACGCACTTA	CTAAGATCTT	700
TAA					703

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE:
 (A) DESCRIPTION: protein
 (iii) HYPOTHETICAL: no
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Leu	Leu	Glu	Thr	Ile	Tyr	Glu	Gly	Leu	Glu	Ser	Ala	Gly	Leu	
				5					10					15	
Thr	Ile	Lys	Gly	Leu	Gln	Gly	Ser	Gln	Thr	Ala	Val	Tyr	Val	Gly	
				20					25					30	
Leu	Met	Ala	Gly	Asp	Tyr	Tyr	Asp	Ile	Gln	Met	Arg	Asp	Ile	Glu	
				35					40					45	
Thr	Leu	Pro	Arg	Tyr	Ala	Ala	Thr	Gly	Thr	Ala	Arg	Ser	Ile	Met	
				50					55					60	
Ser	Asn	Arg	Val	Ser	Tyr	Phe	Phe	Asp	Trp	Lys	Gly	Pro	Ser	Met	
				65					70					75	
Thr	Ile	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ala	Val	His	Gln	
				80					85					90	
Ala	Val	Glu	Ile	Leu	Arg	Arg	Gly	Asp	Val	Thr	Met	Ala	Val	Ala	
				65					70					75	
Ala	Gly	Ala	Asn	Leu	Ile	Tyr	Gly	Pro	Glu	Ala	Tyr	Ile	Ser	Glu	
				110					115					120	
Ser	Asn	Leu	Asn	Met	Leu	Ser	Pro	Ser	Gly	Arg	Ser	Arg	Met	Trp	
				125					130					135	
Asp	Ser	Ser	Ala	Asp	Gly	Tyr	Gly	Arg	Gly	Glu	Gly	Phe	Ala	Ala	
				140					145					150	
Val	Met	Leu	Lys	Thr	Leu	Ser	Ala	Ala	Ile	Arg	Asp	Gly	Asp	His	
				155					160					165	
Ile	Glu	Cys	Ile	Ile	Arg	Glu	Thr	Gly	Ile	Asn	Gln	Asp	Gly	Arg	
				170					175					180	
Thr	Ala	Gly	Ile	Thr	Met	Pro	Ser	Ala	Val	Ser	Gln	Thr	Arg	Leu	
				185					190					195	
Ile	Lys	Asp	Thr	Tyr	Ala	Arg	Ala	Gly	Leu	Asp	Cys	Arg	Lys	Glu	
				200					205					210	
Ala	Glu	Arg	Cys	Gln	Tyr	Phe	Glu	Gly	Lys	Arg	Ile	Thr	Phe	Leu	
				215					220					225	
Asp	Lys	Arg	Thr	Tyr	Xaa	Asp	Leu	Xaa							
				230											

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH:643

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

GCTGTTGCTG GAGGTAAGTT GGGAAGCTTT AGAAAATGCT GGCAAAGCAC 50
CTGAAAAGCT AGCAGGAAGC AATACAGGTG TATTGTGTTGG CATTAGCAAC 100
TTTGATTATT CACAGTTGCA AATTAATCAA ACCGCTCAAC TAGATGCCTA 150
TACAGGCACCT GGCAATGCTT TTAGCATCGC AGCTAACCGT CTTTCCTATT 200
TTCTAGACTT GCACGGACCT AGCTGGGCAG TAGACACAGC CTGTTTCATCA 250
TCTCTAGTAG CAGTCCATCA AGCTTGCCAA AGTCTGCGTC AAGGAGAATG 300
CGAACTAGCC CTCGCTGGTG GTGTAAATCT GATTCTCACC CCACAATTAA 350
CCATCACTTT TTCCCAAGCT GGGATGATGG CTGCTGATGG TCGTTGCAAA 400
ACCTTTGATG CTGATGCTGA TGGTTACGTG CGGGGCGAAG GTTGTGGTGT 450
TGTAATTCTC AAGCGTTTGG CCAACGCTCA ACGAGATGGA GACAATATTT 500
TGGCAGTTAT TAAAGGTTTCG GCAGTTAACC AAGATGGTCG CAGCAACGGA 550
TTGACAGCAC CCAACGGTCA TGCCCAACAA GCAGTTATTC GCCAAGCATT 600
ACAAAATGCC AATGTTGCAG CTGCCGAGAT TAGCTATGTA GAA 643

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Leu Leu Leu Glu Val Ser Trp Glu Ala Leu Glu Asn Ala Gly Lys
      5                      10                      15

Ala Pro Glu Lys Leu Ala Gly Ser Asn Thr Gly Val Phe Val Gly
      20                      25                      30

Ile Ser Asn Phe Asp Tyr Ser Gln Leu Gln Ile Asn Gln Thr Ala
      35                      40                      45

Gln Leu Asp Ala Tyr Thr Gly Thr Gly Asn Ala Phe Ser Ile Ala
      50                      55                      60

Ala Asn Arg Leu Ser Tyr Phe Leu Asp Leu His Gly Pro Ser Trp
      65                      70                      75

Ala Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln
      80                      85                      90

Ala Cys Gln Ser Leu Arg Gln Gly Glu Cys Glu Leu Ala Leu Ala
      95                      100                     105

```

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Gly	Gly	Val	Asn	Leu	Ile	Leu	Thr	Pro	Gln	Leu	Thr	Ile	Thr	Phe
			110						115					120
Ser	Gln	Ala	Gly	Met	Met	Ala	Ala	Asp	Gly	Arg	Cys	Lys	Thr	Phe
			125						130					135
Asp	Ala	Asp	Ala	Asp	Gly	Tyr	Val	Arg	Gly	Glu	Gly	Cys	Gly	Val
			140						145					150
Val	Ile	Leu	Lys	Arg	Leu	Ala	Asn	Ala	Gln	Arg	Asp	Gly	Asp	Asn
			155						160					165
Ile	Leu	Ala	Val	Ile	Lys	Gly	Ser	Ala	Val	Asn	Gln	Asp	Gly	Arg
			170						175					180
Ser	Asn	Gly	Leu	Thr	Ala	Pro	Asn	Gly	His	Ala	Gln	Gln	Ala	Val
			185						190					195
Ile	Arg	Gln	Ala	Leu	Gln	Asn	Ala	Asn	Val	Ala	Ala	Ala	Glu	Ile
			200						205					210

Ser Tyr Val Glu

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 655

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

TCTTTTTTTTG GAGTGTGCTT GGGGAAGCGCT GGAAAATGCT GGTTATGACC 50
CGAAAACAGA CAAAAATCTA ATTGGCGTTT ATGCAGGGGG GAATCTAAGT 100
ACCTACTTAC TTAACAATCT CGCCTCACAC CCTGAACTCA TTAAAGCGCT 150
GGAGTCACAA ATTACAATTG CTAATGATAA GGACTTTATA TGCACACGAG 200
TTTCTTACAA ATTAAACCTG AAAGGGCCGA GTATTAGTGT CGGCACGGCC 250
TGCTCTACGT CATTAGTAGC AGTTCACCTG GCATGTGCGAG GATTGCTAAG 300
TTACCAAGTGT GATATGGCAC TGGCTGGCGG TATTGCGATA CAAGTTCCAC 350
AAAAACAAGG TTATTTCTAT CAAGAAGGTG GCATGGCCTC TCCTGATGGC 400
CACTGTCGGG CCTTTGATGC TAAAGCACAA GGTAGCCCTT TTGGCAAAGG 450
AGCAGGTATT GTCGTGCTGA AAAGATTGGA AGATGCTGTA GCTGATGGAG 500
ACTGCATTTA TGCGGTTATC AAAGGTTTCA CCATCAATAA CGACGGTTCC 550
GAGAAGGTGA GTTACACCGC ACCCAGTGTA ACAGGCCAAG CAGAAGTGAT 600
TGCCGAGGCT CAGGCGATCG CTAACCTTTGA TTCTGAAACA ATCACCTACA 650
TTGAA

```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- 59 -

(A) LENGTH: 217
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE:
 (A) DESCRIPTION: protein
 (iii) HYPOTHETICAL: no
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
 Leu Phe Leu Glu Cys Ala Trp Glu Ala Leu Glu Asn Ala Gly Tyr
 5 10 15
 Asp Pro Lys Thr Asp Lys Asn Leu Ile Gly Val Tyr Ala Gly Gly
 20 25 30
 Asn Leu Ser Thr Tyr Leu Leu Asn Asn Leu Ala Ser His Pro Glu
 35 40 45
 Leu Ile Lys Ala Leu Glu Ser Gln Ile Thr Ile Ala Asn Asp Lys
 50 55 60
 Asp Phe Ile Cys Thr Arg Val Ser Tyr Lys Leu Asn Leu Lys Gly
 65 70 75
 Pro Ser Ile Ser Val Gly Thr Ala Cys Ser Thr Ser Leu Val Ala
 80 85 90
 Val His Leu Ala Cys Arg Gly Leu Leu Ser Tyr Gln Cys Asp Met
 95 100 105
 Ala Leu Ala Gly Gly Ile Ala Ile Gln Val Pro Gln Lys Gln Gly
 110 115 120
 Tyr Phe Tyr Gln Glu Gly Gly Met Ala Ser Pro Asp Gly His Cys
 125 130 135
 Arg Ala Phe Asp Ala Lys Ala Gln Gly Ser Pro Phe Gly Lys Gly
 140 145 150
 Ala Gly Ile Val Val Leu Lys Arg Leu Glu Asp Ala Val Ala Asp
 155 160 165
 Gly Asp Cys Ile Tyr Ala Val Ile Lys Gly Ser Ala Ile Asn Asn
 170 175 180
 Asp Gly Ser Glu Lys Val Ser Tyr Thr Ala Pro Ser Val Thr Gly
 185 190 195
 Gln Ala Glu Val Ile Ala Glu Ala Gln Ala Ile Ala Asn Phe Asp
 200 205 210
 Ser Glu Thr Ile Thr Tyr Ile
 215

(2) INFORMATION FOR SEQ ID NO:57:

- 60 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

ATTGCTGCTT GAAAACGTCT ATGAAGCTCT TGAAAACGGT GAGCGGTTCT 50
TCAAGAGAAT ATTGATGCAT CAATATGCTA ACTTGATGTC AATCATCAGC 100
TGGTATTCCT CTGAGCGAGT CCGTCTCTTC TAACACCTCC GTTTATGTTG 150
GCTCATTCGG TGATGACTAT AAGACGATTC TCAATACCGA TTTTGAGAGT 200
TGGGTCAAGT ACAAAGGCAC CGGTGTCTAT AACTCGATTC TGGCCAATCG 250
AATCAGCTGG TTCTACGACT TTAAAGGAGC CAGCGTCACG CTAGATACCG 300
CATGCTCGAG TAGCTTG GTA GCCGTGCATA TGGCTTGCCA GGATTTGAGG 350
TTGGGAGAGT CTAGAATGGT CAGTGTATTT CTCTATTGAA AAGTACTAGA 400
GGATTCTAAT TGACGTATTT GGATACCACT CCGTTGTCTCGG CCGGTGTCAAC 450
ATCATTGGCC ATCCGTTGCT CGTCCACGAT CTAAGCAAGC TCGGAGCGCT 500
CTCTCCTGAT GCGTGTGCT ACACTTTCGA TGAACGGGCC AATGGATATT 550
CCCGGGGAGA AGGTGTCTGGC ACCATCGTTC TCAAACGGCT CTCTGACGCA 600
ATCGAAGATG GTGATACCAT TCGCGCTATC ATCCGTGCAA GCGGGTGCAA 650
TCAAGACGGT AAAACAGCAG GTATATTGT CCCTTCAGTC CAAGCCCAGG 700
AGCGACTTAT CCGGGATACC TATGAGAAGG CTGGGCTTGA CCGGACACGC 750
ACGACATATT TGAA

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Leu Leu Leu Glu Asn Val Tyr Glu Ala Leu Glu Asn Ala Gly Ile
      5                      10                      15

Pro Leu Ser Glu Ser Val Ser Ser Asn Thr Ser Val Tyr Val Gly
      20                      25                      30

Ser Phe Gly Asp Asp Tyr Lys Thr Ile Leu Asn Thr Asp Phe Glu
      35                      40                      45

Ser Trp Val Lys Tyr Lys Gly Thr Gly Val Tyr Asn Ser Ile Leu
      50                      55                      60

Ala Asn Arg Ile Ser Trp Phe Tyr Asp Phe Lys Gly Ala Ser Val
      65                      70                      75

Thr Leu Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Met
      80                      85                      90

```

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Ala	Cys	Gln	Asp	Leu	Arg	Leu	Gly	Glu	Ser	Arg	Met	Val	Ser	Ser	
				95					100					105	
Val	Val	Gly	Gly	Val	Asn	Ile	Ile	Gly	His	Pro	Leu	Leu	Val	His	
				110					115					120	
Asp	Leu	Ser	Lys	Leu	Gly	Ala	Leu	Ser	Pro	Asp	Gly	Val	Cys	Tyr	
				125					130					135	
Thr	Phe	Asp	Glu	Arg	Ala	Asn	Gly	Tyr	Ser	Arg	Gly	Glu	Gly	Val	
				140					145					150	
Gly	Thr	Ile	Val	Leu	Lys	Arg	Leu	Ser	Asp	Ala	Ile	Glu	Asp	Gly	
				155					160					165	
Asp	Thr	Ile	Arg	Ala	Ile	Ile	Arg	Ala	Ser	Gly	Cys	Asn	Gln	Asp	
				170					175					180	
Gly	Lys	Thr	Ala	Gly	Ile	Phe	Val	Pro	Ser	Val	Gln	Ala	Gln	Glu	
				185					190					195	
Arg	Leu	Ile	Arg	Asp	Thr	Tyr	Glu	Lys	Ala	Gly	Leu	Asp	Arg	Thr	
				200					205					210	
Arg	Thr	Thr	Tyr	Leu	Glu										
				215											

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TAAGTTACTG	GAAACAGCAT	ATACTGCGTT	TGAGAACGGT	GAGTACGCCT	50
TGCGTCGTAT	CCCCTCCCCC	CTCATGGAAG	ATCTCAATCT	GATCTCGTGA	100
AACAGCCGGC	ATCGGGTTAG	AAGCGGCACG	AGGATCAAAC	ACTTCAGTAC	150
ATATAGGTTG	TTTTAATATC	GACTATACAA	GCAACCATAG	TAGAGATCCA	200
GAGCAGATGC	ACAAATATAC	GGGGACTGGA	GGAGCACCTT	CCATGCTGTC	250
GAACAGACTG	AGTTGGTTTT	TCGATCTGAG	AGGACCGAGC	TTGACCTTGG	300
ACACGGCATG	CTCTAGTAGC	ATGGTTGCGC	TTGATTTAGC	ATGCCAGACT	350
TTGCAAAGTG	GACAATCTGA	CATGGGTCTT	GTCGGGGGTT	GTAATCTCAT	400
CTACAGCGTC	GACATGACCA	TGGCTCTATC	CAAGCTTGGA	TTTCTCTCCC	450
ATAACAGTCG	GTGCTACAGT	TTTGACCATC	GAGCGGATGG	GTACGCCAGA	500
GGTGAAGGCT	TTGGAGTTTT	AATTCTCAAA	CGTGTCGAAG	ACGCCATACG	550
AGATGGGGAT	ACTATACGAG	GAGTCATTCG	ATTAACAAGC	TCCAATCAAG	600
ACGGCCATAC	TCCGGGAATA	ACAATGCCCA	GCAGAGACGC	CCAAGCAAGT	650
TTGATTAGAA	AGACATACCA	ACAAGCTGGA	TTAGATATGC	AGATGACAGG	700
CTACTTTGA					709

(2) INFORMATION FOR SEQ ID NO:60:

- 62 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Lys	Leu	Leu	Glu	Thr	Ala	Tyr	Thr	Ala	Phe	Glu	Asn	Ala	Gly	Ile	5	10	15
Gly	Leu	Glu	Ala	Ala	Arg	Gly	Ser	Asn	Thr	Ser	Val	His	Ile	Gly	20	25	30
Cys	Phe	Asn	Ile	Asp	Tyr	Thr	Ser	Asn	His	Ser	Arg	Asp	Pro	Glu	35	40	45
Gln	Met	His	Lys	Tyr	Thr	Gly	Thr	Gly	Gly	Ala	Pro	Ser	Met	Leu	50	55	60
Ser	Asn	Arg	Leu	Ser	Trp	Phe	Phe	Asp	Leu	Arg	Gly	Pro	Ser	Leu	65	70	75
Thr	Leu	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Met	Val	Ala	Leu	Asp	Leu	80	85	90
Ala	Cys	Gln	Thr	Leu	Gln	Ser	Gly	Gln	Ser	Asp	Met	Gly	Leu	Val	95	100	105
Gly	Gly	Cys	Asn	Leu	Ile	Tyr	Ser	Val	Asp	Met	Thr	Met	Ala	Leu	110	115	120
Ser	Lys	Leu	Gly	Phe	Leu	Ser	His	Asn	Ser	Arg	Cys	Tyr	Ser	Phe	125	130	135
Asp	His	Arg	Ala	Asp	Gly	Tyr	Ala	Arg	Gly	Glu	Gly	Phe	Gly	Val	140	145	150
Leu	Ile	Leu	Lys	Arg	Val	Glu	Asp	Ala	Ile	Arg	Asp	Gly	Asp	Thr	155	160	165
Ile	Arg	Gly	Val	Ile	Arg	Leu	Thr	Ser	Ser	Asn	Gln	Asp	Gly	His	170	175	180
Thr	Pro	Gly	Ile	Thr	Met	Pro	Ser	Arg	Asp	Ala	Gln	Ala	Ser	Leu	185	190	195
Ile	Arg	Lys	Thr	Tyr	Gln	Gln	Ala	Gly	Leu	Asp	Met	Gln	Met	Thr	200	205	210

Gly Tyr Phe

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- 63 -

- (A) LENGTH: 649
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

AATGTTGCTC GAGATCACCT ACGAAGCCCT GGAGAACGCT GGA CTTCCTT 50
TGAGTAAGGT TGTCGGCTCT GATACAGCCT GCTTCATTGG TGGCTTTACA 100
CGAATTATG ATGATTTGAC CACTTCGGAG CTCGCGAAGA CCCTACTCTA 150
CACAACTACC GGCAACGGCC TGACGATGAT GTCGAATCGC TTATCCTGGT 200
TCTACGACCT TCATGGCCCG TCGGTTTCGC TCGACACAGC ATGTTCTAGC 250
TCGCTGGTTG CACTAAACCT TGCATGCCAG ACAATCCGAG CATCGACGAA 300
TGACTCTCGA CAGGCGATAG TTGGAGGTGT CAATCTCATG CTGCTCCCTG 350
ATCAGATGAC CACGATTAAT CCTCTGCATT TCTTAAGTCC TGATAGCCAA 400
TGCTACTCGT TTGATGACCG TGCAAACGGT TACACCCGTG GAGAAGGTAT 450
TGGCATACTG GTGCTCAAGC ACATCAATGA TGCTATTCTGA GATGGAGACT 500
GTATAAGGGC AGTAATCCGC GGCACCTGGGG TCAACTCCGA TGGCAAGACC 550
CCTGGCATT CCTTGCCAAG CACGGCTGCA CAAGCCTCTT TAATTCGCGC 600
AACGTACGCC TCGGCAGGGC TGGACCCAGC TCACACCGGC TACTTTGAA 649
  
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Met Leu Leu Glu Ile Thr Tyr Glu Ala Leu Glu Asn Ala Gly Leu
      5                      10                      15

Pro Leu Ser Lys Val Val Gly Ser Asp Thr Ala Cys Phe Ile Gly
      20                      25                      30

Gly Phe Thr Arg Asp Tyr Asp Asp Leu Thr Thr Ser Glu Leu Ala
      35                      40                      45

Lys Thr Leu Leu Tyr Thr Thr Thr Gly Asn Gly Leu Thr Met Met
      50                      55                      60

Ser Asn Arg Leu Ser Trp Phe Tyr Asp Leu His Gly Pro Ser Val
      65                      70                      75

Ser Leu Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu Asn Leu
      80                      85                      90

Ala Cys Gln Thr Ile Arg Ala Ser Thr Asn Asp Ser Arg Gln Ala
      95                      100                     105

Ile Val Gly Gly Val Asn Leu Met Leu Leu Pro Asp Gln Met Thr
      110                     115                     120
  
```

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Thr	Ile	Asn	Pro	Leu	His	Phe	Leu	Ser	Pro	Asp	Ser	Gln	Cys	Tyr
				125					130					135
Ser	Phe	Asp	Asp	Arg	Ala	Asn	Gly	Tyr	Thr	Arg	Gly	Glu	Gly	Ile
				140					145					150
Gly	Ile	Leu	Val	Leu	Lys	His	Ile	Asn	Asp	Ala	Ile	Arg	Asp	Gly
				155					160					165
Asp	Cys	Ile	Arg	Ala	Val	Ile	Arg	Gly	Thr	Gly	Val	Asn	Ser	Asp
				170					175					180
Gly	Lys	Thr	Pro	Gly	Ile	Thr	Leu	Pro	Ser	Thr	Ala	Ala	Gln	Ala
				185					190					195
Ser	Leu	Ile	Arg	Ala	Thr	Tyr	Ala	Ser	Ala	Gly	Leu	Asp	Pro	Ala
				200					205					210
His	Thr	Gly	Tyr	Phe	Glu									
				215										

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TATGCTACTT	GAATGCACAT	ACGAAGCGTT	AGAGAATGGT	CAGTGAGCTA	50
CGAGCCGATT	TTCATATATC	ATGGCTAACA	AGTTGAAGCT	GGCATAACCTC	100
TAGATAAAGT	AGTAGGAGAA	CCCGTAGGGG	TGTACGTCGG	CTCAGCTAGT	150
TCCGATTACT	CGGACATCGT	GAACTCAGAC	GGCGAGATGG	TCTCCACTTA	200
CACGGCCACG	GGGTTGGCCG	CAACGATGAT	GGCAAACCGC	ATATCCTATT	250
TCTATGATCT	CCGGGGGCCA	AGCTTCACAT	TGGACACGGC	GTGTTCATCG	300
AGTTTGATGG	CGTTACACCT	AGCGTGCCAA	AGTCTTCGAG	TCGGTGAATC	350
GAAGCAAGCC	ATTGTGGGCG	GGGTCCACCT	TGTACTGAGC	CCGGATTGTA	400
TGACTTCGAT	GAGTTTATTA	GGGTAAGACC	TTCAAAATCT	CCATGCAGAA	450
TTTCTAAATC	TAACCTACCA	CCCTAGTTTG	TTCTCTAATG	ACGGCCGATC	500
CTACACTTAT	GACCATCGAG	GTAAGGTTTA	TGGGCGCGGC	GAAGGTATTG	550
CTACCTTAGT	AATAAAACCT	CTTAAAGATG	CGATGGAAGC	CGGTGATAAC	600
ATCCGGGCCA	TCATCCGCAA	TAGTGGGGCA	AATCAAGATG	GTCGAACACC	650
AGGTGTGACT	TTTCCAAGTC	AAGATGCTCA	GATAGATCTT	ATGAGATCGG	700
TATATCGTTC	CGCTGGACTT	GATGTACTTG	ATACCGGCTA	CGTGGAA	747

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- 65 -

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Met Leu Leu Glu Cys Thr Tyr Glu Ala Leu Glu Asn Ala Gly Ile
      5              10              15
Pro Leu Asp Lys Val Val Gly Glu Pro Val Gly Val Tyr Val Gly
      20              25              30
Ser Ala Ser Ser Asp Tyr Ser Asp Ile Val Asn Ser Asp Gly Glu
      35              40              45
Val Ser Thr Tyr Thr Ala Thr Gly Leu Ala Ala Thr Met Met
      50              55              60
Ala Asn Arg Ile Ser Tyr Phe Tyr Asp Leu Arg Gly Pro Ser Phe
      65              70              75
Thr Leu Asp Thr Ala Cys Ser Ser Ser Leu Met Ala Leu His Leu
      80              85              90
Ala Cys Gln Ser Leu Arg Val Gly Glu Ser Lys Gln Ala Ile Val
      95              100             105
Gly Gly Val His Leu Val Leu Ser Pro Asp Cys Met Thr Ser Met
      110             115             120
Ser Leu Leu Gly Leu Phe Ser Asn Asp Gly Arg Ser Tyr Thr Tyr
      125             130             135
Xaa His Arg Gly Thr Gly Tyr Gly Arg Gly Xaa Gly Ile Ala Thr
      140             145             150
Leu Val Ile Lys Pro Leu Lys Asp Ala Met Glu Ala Gly Asp Asn
      155             160             165
Ile Arg Ala Ile Ile Arg Asn Ser Gly Ala Asn Gln Asp Gly Arg
      170             175             180
Thr Pro Gly Val Thr Phe Pro Ser Gln Asp Ala Gln Ile Asp Leu
      185             190             195
Met Arg Ser Val Tyr Arg Ser Ala Gly Leu Asp Val Leu Asp Thr
      200             205             210
Gly Tyr Val Glu

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 66 -

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

```

AATTCTACTT GAAGTCGCCT ATCAAGCAAT GGAGTCAAGC GGCTGCTTAC 50
GGAACCATCG ACGCGAAGCT GGGGATCCTG TGGGATGTTT TATTGGAGCT 100
AGCTTTGCCG AATATCTTGA CAACACCTGT TCTAATCCGC CAACCAGCTA 150
TACTTCCACT GGCACCATCA GAGCTTTCCA CTGCGGTAGA CTCAGTTATT 200
ACTTTGGATG GAGCGGTCCT GCCGAGGTCA TTGATACAGC TTGCTCCTCT 250
TCGTTGGTTG CTATCAATCG AGCTTGCAAG TCAGTGCAGG CGGGTGAATG 300
TACAATGGCT CTTACTGGTG GAGTGAACAT TATAACTGGT ATCCACAAC 350
TCTTAGATCT GGCAAAGGCT GGCTTYTTAA GCCCCACAGG CCAATGCAGA 400
CCCTTTGACC AGTCTGCAGA TGGGTATTGT CGCTCAGAAG GAGCAGGACT 450
TGTTGTACTA AACTGTGTTAA GCCAAGCCAT AGCAGATGGA GATCAAATTT 500
TCGGAGTTAT TCCAAGTGTG TCCACCAACC AAGGCGGATT GTCATCTTCA 550
ATTACGATTC CTCATTCGCC TGCACAAAAA AAGTTGTATC AAACCGTGCT 600
TCGGCAAGCC GGCATGAAGC TAGAACAGGT TAGCTACGTA GAG 643

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Ile Leu Leu Glu Val Ala Tyr Gln Ala Met Glu Ser Ser Gly Cys
      5                      10                      15

Leu Arg Asn His Arg Arg Glu Ala Gly Asp Pro Val Gly Cys Phe
      20                      25                      30

Ile Gly Ala Ser Phe Ala Glu Tyr Leu Asp Asn Thr Cys Ser Asn
      35                      40                      45

Pro Pro Thr Ser Tyr Thr Ser Thr Gly Thr Ile Arg Ala Phe His
      50                      55                      60

Cys Gly Arg Leu Ser Tyr Tyr Phe Gly Trp Ser Gly Pro Ala Glu
      65                      70                      75

Val Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile Asn Arg
      80                      85                      90

Ala Cys Lys Ser Val Gln Ala Gly Glu Cys Thr Met Ala Leu Thr
      95                      100                     105

Gly Gly Val Asn Ile Ile Thr Gly Ile His Asn Phe Leu Asp Leu
      110                     115                     120

Ala Lys Ala Gly Phe Leu Ser Pro Thr Gly Gln Cys Arg Pro Phe
      125                     130                     135

```

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Asp	Gln	Ser	Ala	Asp	Gly	Tyr	Cys	Arg	Ser	Glu	Gly	Ala	Gly	Leu
				140					145					150
Val	Val	Leu	Lys	Leu	Leu	Ser	Gln	Ala	Ile	Ala	Asp	Gly	Asp	Gln
				155					160					165
Ile	Phe	Gly	Val	Ile	Pro	Ser	Val	Ser	Thr	Asn	Gln	Gly	Gly	Leu
				170					175					180
Ser	Ser	Ser	Ile	Thr	Ile	Pro	His	Ser	Pro	Ala	Gln	Lys	Lys	Leu
				185					190					195
Tyr	Gln	Thr	Val	Leu	Arg	Gln	Ala	Gly	Met	Lys	Leu	Glu	Gln	Val
				200					205					210

Ser Tyr Val Glu

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 809

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

AGGAAACTAC TAGAGGTCGT GTTTGAATGT TTTGAGAGTG CCGGTACACC 50
ACTTCACGCA GTTTCAGGAG CTAATATTGG CTGCTATGTT GGGAATTTTA 100
CGTTGGATTA TCTTGTCATG CAGTCTAAGG ATACAGACTC TTTTCATCGA 150
TATACTGCTC CAGGAATGGG ACCTACATTG TTAGCTAACC GCATAAGTCA 200
TGTTTTTAAT CTTCAAGGTC CAAGTGTTAT GCTTGATACA GCGTGTTCTT 250
CATCGATCTA CGCTCTTCAT GCAGCTTGTG TGGCCTTGAA TGCAGATGAG 300
TGCAATGCAG CAATTGTTGC TGGGGCAAAC CTAATCCAGT CACCTGAGTG 350
GCATCTTGCA GTCTCCAAAT CAGGTGTGAT TTCACAAACT TCCACGTGTC 400
ACACTTTTCA TGCTAGTGCG GATGGTTATG GGCGAGGCGA GGGCGTTGGG 450
GCCCTCTATC TCAAGCGTCT AAGTGACGCA ATCCGAGATC GAGATCCTAT 500
ACGGTCTGTT ATTCGTGGTA CAGCTGTAA TAGGTTAGTA CATCCTCTTA 550
CCTTTCTTTC ATGGATTAGC GAGAATTAGG GTTCCAAATG TTTGAAAGCT 600
CGGGTTCTAA TATTCATTCA CTGGACTAGT AATGGCAAGA CAAACGGCAT 650
CAGTCAGCCT AGTGCTTTGG CACAGGAAGC TGTGATTAAA AAAGCTTATG 700
CAAAGGCGGG ATTACCTGTT ACCGAGACTG ACTATGTTGA GGTAAGTGAG 750
CTATGTTTAA ATCAGAAAAC GTCATGCCAT TATTTCTTAT CCTTCACTGA 800
NCTCTTACA                                     809

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

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(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Arg	Lys	Leu	Leu	Glu	Val	Val	Phe	Glu	Cys	Phe	Glu	Ser	Ala	Gly	5	10	15
Thr	Pro	Leu	His	Ala	Val	Ser	Gly	Ala	Asn	Ile	Gly	Cys	Tyr	Val	20	25	30
Gly	Asn	Phe	Thr	Leu	Asp	Tyr	Leu	Val	Met	Gln	Ser	Lys	Asp	Thr	35	40	45
Asp	Ser	Phe	His	Arg	Tyr	Thr	Ala	Pro	Gly	Met	Gly	Pro	Thr	Leu	50	55	60
Leu	Ala	Asn	Arg	Ile	Ser	His	Val	Phe	Asn	Leu	Gln	Gly	Pro	Ser	65	70	75
Val	Met	Leu	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Ile	Tyr	Ala	Leu	His	80	85	90
Ala	Ala	Cys	Val	Ala	Leu	Asn	Ala	Asp	Glu	Cys	Asn	Ala	Ala	Ile	95	100	105
Val	Ala	Gly	Ala	Asn	Leu	Ile	Gln	Ser	Pro	Glu	Trp	His	Leu	Ala	110	115	120
Val	Ser	Lys	Ser	Gly	Val	Ile	Ser	Gln	Thr	Ser	Thr	Cys	His	Thr	125	130	135
Phe	Asp	Ala	Ser	Ala	Asp	Gly	Tyr	Gly	Arg	Gly	Glu	Gly	Val	Gly	140	145	150
Ala	Leu	Tyr	Leu	Lys	Arg	Leu	Ser	Asp	Ala	Ile	Arg	Asp	Arg	Asp	155	160	165
Pro	Ile	Arg	Ser	Val	Ile	Arg	Gly	Thr	Ala	Val	Asn	Ser	Asn	Gly	170	175	180
Lys	Thr	Asn	Gly	Ile	Ser	Gln	Pro	Ser	Ala	Leu	Ala	Gln	Glu	Ala	185	190	195
Val	Ile	Lys	Lys	Ala	Tyr	Ala	Lys	Ala	Gly	Leu	Pro	Val	Thr	Glu	200	205	210
Thr	Asp	Tyr	Val	Glu	Val	Ser	Glu	Leu	Cys	Leu	Asn	Gln	Lys	Thr	215	220	225
Ser	Cys	His	Tyr	Phe	Leu	Ser	Phe	Thr	Xaa	Leu	Leu				230	235	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 658

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

TTTGCTCCTT GAGACTGTCT ACGAAGCTCT GGAAGCAGGC GGTCACACGA 50
TTGAAGCGCT ACGAGGATCT GATACGTCTG TCTTTACAGG CACCATGGGC 100
GTCGACTACA ACGATACTGT TATACGGGAC CTGAACGTCA TCCCGACGTA 150
CTTTGCTACT GGAGTAAATC GAGCTATCAT CTCGAACCGA GTCTCATACT 200
TCTTTGACTG GCATGGGCCG AGCATGACCA TCGACACAGC CTGTTTCATCC 250
AGTCTCGTCG CCGTGCACCA AGGAGTGAAA GCTCTTCGGA GTGGGGAGTC 300
GCGTACTGCC CTGGCATGTG GGACGCAGGT CATTCTAAAT CCCGAGATGT 350
ATGTTATTGA GAGCAAGCTG AAAATGCTTT CTCCTACGGG CCGCTCCCGC 400
ATGTGGGATG CGGACGCGGA TGGCTACGCT CGTGGGGAGG GCGTAGCGGC 450
TGTAGTGCTG AAACGGCTCA GTGACGCTAT TGC GGATGGA SATCGCATCG 500
AGTGCATCAT CCGTGAGACA GGGTCCAACC AAGACGGCCA TTCAAATGGT 550
ATCACGGTGC CGAGTACGGA GGCCCAAGCG GCCCTCATCC ACCAAACCTA 600
TGCCAGAGCT GGTCTAGACC CGGAAAATAA CCCTCACGAC CGCCCTCAGT 650
TCTTCGAA                                     658
  
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Leu Leu Leu Glu Thr Val Tyr Glu Ala Leu Glu Ala Gly Gly His
      5                      10                      15

Thr Ile Glu Ala Leu Arg Gly Ser Asp Thr Ser Val Phe Thr Gly
      20                      25                      30

Thr Met Gly Val Asp Tyr Asn Asp Thr Val Ile Arg Asp Leu Asn
      35                      40                      45

Val Ile Pro Thr Tyr Phe Ala Thr Gly Val Asn Arg Ala Ile Ile
      50                      55                      60

Ser Asn Arg Val Ser Tyr Phe Phe Asp Trp His Gly Pro Ser Met
      65                      70                      75

Thr Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln
      80                      85                      90

Gly Val Lys Ala Leu Arg Ser Gly Glu Ser Arg Thr Ala Leu Ala
      95                      100                     105

Cys Gly Thr Gln Val Ile Leu Asn Pro Glu Met Tyr Val Ile Glu
      110                     115                     120
  
```

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Ser	Lys	Leu	Lys	Met	Leu	Ser	Pro	Thr	Gly	Arg	Ser	Arg	Met	Trp
				125					130					135
Asp	Ala	Asp	Ala	Asp	Gly	Tyr	Ala	Arg	Gly	Glu	Gly	Val	Ala	Ala
				140					145					150
Val	Val	Leu	Lys	Arg	Leu	Ser	Asp	Ala	Ile	Ala	Asp	Gly	---	Arg
				155					160					165
Ile	Glu	Cys	Ile	Ile	Arg	Glu	Thr	Gly	Ser	Asn	Gln	Asp	Gly	His
				170					175					180
Ser	Asn	Gly	Ile	Thr	Val	Pro	Ser	Thr	Glu	Ala	Gln	Ala	Ala	Leu
				185					190					195
Ile	His	Gln	Thr	Tyr	Ala	Arg	Ala	Gly	Leu	Asp	Pro	Glu	Asn	Asn
				200					205					210
Pro	His	Asp	Arg	Pro	Gln	Phe	Phe	Glu						
				215										

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGGGCTACTC	GAGACTGCTT	ACAAGGCGTT	CGAAAACGGT	GAGTCTTGAA	50
GCTGCACAGA	TCAAGACAAG	AACACTAAAT	CTCTCAGCGG	GCATACGCAT	100
AGAAGAAGCC	GCTGGCTCTA	GAACCTCAGT	TCATATCGGG	AGTTTCACTC	150
ATGATTGGAG	AGACATCCTC	CAAAGGGATC	CACTAATGGA	TGTTAGCTAC	200
ATAGCTACCG	CAACCGAGGT	TTCTATGCTA	GCGAGTCGAC	TCAGCTGGTT	250
TTATGATCTA	AGTGGGCCYA	GCATCTCCTT	GGATACAGCG	TGTTTCGAGTA	300
GCTTAATGGC	TTTACATCTC	GCCTGCCAGA	GTCTAAAGAG	TCGAGAGGCC	350
GACATGGTAA	GGCTATGCTA	CTTTCTGGCT	CACTCAAAC	GTTTTCCATA	400
TCTGATGCTT	GCACAGGGCC	TTGTTGGGAG	GGGCTAATCT	TCTTTTGGAT	450
CCTGTAGGGG	TTATTGGCAT	AACAAATGTT	GGCATGCTTT	CGCCAGATGG	500
CATTAGTTAC	AGCTTTGATC	ATCGTGCAAA	CGGGTATGCC	CGAGGAGAAG	550
GGTTCGAGT	CGTTGTCATC	AAACGCTTGG	ACGATGCTCT	CAGACATGGC	600
GATACTATTC	GCGGTATCGT	TCGTGCCACA	GGATCGAATC	AAGATGGAAG	650
AACTCCAGGG	ATTACCCAAC	CTGATGGAGC	CGCGCAAGAA	GAGCTCATCC	700
GAGACACTTA	CAAAGCTGCT	GGCTTAGATA	TGAGGCTAGT	AAGGTATTCT	750
TAA					753

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly	Leu	Leu	Glu	Thr	Ala	Tyr	Lys	Ala	Phe	Glu	Asn	Ala	Gly	Ile	5	10	15
Arg	Ile	Glu	Glu	Ala	Ala	Gly	Ser	Arg	Thr	Ser	Val	His	Ile	Gly	20	25	30
Ser	Phe	Thr	His	Asp	Trp	Arg	Asp	Ile	Leu	Gln	Arg	Asp	Pro	Leu	35	40	45
Met	Asp	Val	Ser	Tyr	Ile	Ala	Thr	Ala	Thr	Glu	Val	Ser	Met	Leu	50	55	60
Ala	Ser	Arg	Leu	Ser	Trp	Phe	Tyr	Asp	Leu	Ser	Gly	Pro	Ser	Ile	65	70	75
Ser	Leu	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Met	Ala	Leu	His	Leu	80	85	90
Ala	Cys	Gln	Ser	Leu	Lys	Ser	Arg	Glu	Ala	Asp	Met	Gly	Leu	Val	95	100	105
Gly	Gly	Ala	Asn	Leu	Leu	Leu	Asp	Pro	Val	Gly	Val	Ile	Gly	Ile	110	115	120
Thr	Asn	Val	Gly	Met	Leu	Ser	Pro	Asp	Gly	Ile	Ser	Tyr	Ser	Phe	125	130	135
Asp	His	Arg	Ala	Asn	Gly	Tyr	Ala	Arg	Gly	Glu	Gly	Phe	Gly	Val	140	145	150
Val	Val	Ile	Lys	Arg	Leu	Asp	Asp	Ala	Leu	Arg	His	Gly	Asp	Thr	155	160	165
Ile	Arg	Gly	Ile	Val	Arg	Ala	Thr	Gly	Ser	Asn	Gln	Asp	Gly	Arg	170	175	180
Thr	Pro	Gly	Ile	Thr	Gln	Pro	Asp	Gly	Ala	Ala	Gln	Glu	Glu	Leu	185	190	195
Ile	Arg	Asp	Thr	Tyr	Lys	Ala	Ala	Gly	Leu	Asp	Met	Arg	Leu	Val	200	205	210

Arg Tyr Ser

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:753

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

ATTGTTGCTC GAAGTAACCT ATGAAGCTTT AGAGAACGGT GGGTAGTTCC 50
AGGAAGCATT AATCAAGACA AAGCTATTGC TCACACTTTT CCAAAATAGC 100
CGGAATACCC TTGAACCAAA TTGTGGGCCA GGATGTTGGG GTTTTGTGTTG 150
GCGGCTCAAT GTCCGACTAC CAGAACCTCC TCCACAAAGA CATCGCAAAT 200
GGTCCTATTT ACCAAGCCAC TGGCACTGCC ATGAGCTTCC TAGCCAACCG 250
AATATCTTAC ATCTATGACC TCAAGGGCCC AAGCGTAACA GTGGACACTG 300
CATGCTCCTC GGGTCTCAGC GCACTTCATT TAGCATGCCA GAGCATACGC 350
ACTGGTGAGA TCCGACAAGC TTTGGTCGGC GGTGTATACA TTATCCTAAG 400
CCCGGAGAAT ATGATTGCCA TGAGCATGCT GGGGTGATGT CTCCTGTTCC 450
AGAAAGTAAT TGATAAAAGC TAATGCCAGT AGACTGTTTG GCACCGACGG 500
TCTCTCATAc AGCTATGATC ACCGAGCAAC TGGATATGGA CGTGGTGAAG 550
GAGGAGGCAT GATAGTCTTA AAGTCGCTAG ACGACGCGAT GGCAAACGGA 600
GACACAATAC ATGCGGTAAT TCGGCACACA GGGACAAATC AGGATGGTAA 650
GACCAGCGGC CCAACAATGC CCAGTCTGGA AGCCCAGGAG AGACTCATCA 700
AGAAAGTTTA CAGCCAGGCT GGTCTGGATC CATTGGATAC AGAATATGTC 750
GAG
  
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Leu Leu Leu Glu Val Thr Tyr Glu Ala Leu Glu Asn Ala Gly Ile
      5                      10                      15

Pro Leu Asn Gln Ile Val Gly Gln Asp Val Gly Val Phe Val Gly
      20                      25                      30

Gly Ser Met Ser Asp Tyr Gln Asn Leu Leu His Lys Asp Ile Ala
      35                      40                      45

Asn Gly Pro Ile Tyr Gln Ala Thr Gly Thr Ala Met Ser Phe Leu
      50                      55                      60

Ala Asn Arg Ile Ser Tyr Ile Tyr Asp Leu Lys Gly Pro Ser Val
      65                      70                      75

Thr Val Asp Thr Ala Cys Ser Ser Gly Leu Thr Ala Leu His Leu
      80                      85                      90

Ala Cys Gln Ser Ile Arg Thr Gly Glu Ile Arg Gln Ala Leu Val
      95                      100                     105

Gly Gly Val Tyr Ile Ile Leu Ser Pro Glu Asn Met Ile Ala Met
  
```

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	110		115		120
Ser Met Leu Gly	Leu Phe Gly Thr Asp	Gly Leu Ser Tyr Ser Tyr			
	125	130			135
Asp His Arg Ala	Thr Gly Tyr Gly Arg	Gly Glu Gly Gly Gly Met			
	140	145			150
Ile Val Leu Lys	Ser Leu Asp Asp Ala	Met Ala Asn Gly Asp Thr			
	155	160			165
Ile His Ala Val	Ile Arg His Thr Gly	Thr Asn Gln Asp Gly Lys			
	170	175			180
Thr Ser Gly Pro	Thr Met Pro Ser Leu	Glu Ala Gln Glu Arg Leu			
	185	190			195
Ile Lys Lys Val	Tyr Ser Gln Ala Gly	Leu Asp Pro Leu Asp Thr			
	200	205			210

Glu Tyr Val Glu

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

AATGCTGCTT GAGGTAGTCT ATGAGGCGTT AGAAGACGGT AAGTCTAACG 50
AATTTCAATC AGTGGTCCTG AGCTAATTGC GATCAAGCTG GCATTACGCT 100
CGACGACATT AAGGGTTCCC AGACATCTGT CTACTGTGGG AGCTTCACCA 150
ACGACTACCG TGAAATGCTG AACAAAGATT TGGGGTACTA CCCCAAGTAC 200
ATGGCCACTG GTGTTGAAA CTCCATCTTA GCCAACCGCA TTTCATATTT 250
CTATGACCTA CACGGACCAA GTGTGACTGT CGACACAGCC TGCTCTCTTC 300
CCCTGGTCTC ATTCCATATG GGCAACAGAT CAATCCMAGA TGGAGATGCT 350
GACATCTCAA TCGTCATTGG ATCTTCGCTC CATTTTGATC CCAACATGTT 400
CGTCACTATG ACGGACCTTG GGTTCCTCTC AACCGACGGC AGATGCCGTG 450
CTTTTGACGC TAGCGGAAAG GGGTATGTCC GCGGTGAGGG CATCTGCGCT 500
GTTGTTTTGA AACAAAAATC ACGCGCTGAA CTTACACGACA ACAACGTTTCG 550
ATCCGTCATT CGTGGCTCGG ATGTCAACCA CGACGGTGCC AAAGACGGTA 600
TCACAATGCC AAATCGAAG GCTCAGGAGA GCCTCATCAG AAAGACCTAC 650
AAAAACGCTG GACTGAGTAC AAACGACACC CAGTACTTTG AG 692

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE:
 (A) DESCRIPTION: protein
 (iii) HYPOTHETICAL: no
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Leu	Leu	Glu	Val	Val	Tyr	Glu	Ala	Leu	Glu	Asp	Ala	Gly	Ile	5	10	15
Thr	Leu	Asp	Asp	Ile	Lys	Gly	Ser	Gln	Thr	Ser	Val	Tyr	Cys	Gly	20	25	30
Ser	Phe	Thr	Asn	Asp	Tyr	Arg	Glu	Met	Leu	Asn	Lys	Asp	Leu	Gly	35	40	45
Tyr	Tyr	Pro	Lys	Tyr	Met	Ala	Thr	Gly	Val	Gly	Asn	Ser	Ile	Leu	50	55	60
Ala	Asn	Arg	Ile	Ser	Tyr	Phe	Tyr	Asp	Leu	His	Gly	Pro	Ser	Val	65	70	75
Thr	Val	Asp	Thr	Ala	Cys	Ser	Leu	Pro	Leu	Val	Ser	Phe	His	Met	80	85	90
Gly	Asn	Arg	Ser	Ile	Xaa	Asp	Gly	Asp	Ala	Asp	Ile	Ser	Ile	Val	95	100	105
Ile	Gly	Ser	Ser	Leu	His	Phe	Asp	Pro	Asn	Met	Phe	Val	Thr	Met	110	115	120
Thr	Asp	Leu	Gly	Phe	Leu	Ser	Thr	Asp	Gly	Arg	Cys	Arg	Ala	Phe	125	130	135
Asp	Ala	Ser	Gly	Lys	Gly	Tyr	Val	Arg	Gly	Glu	Gly	Ile	Cys	Ala	140	145	150
Val	Val	Leu	Lys	Gln	Lys	Ser	Arg	Ala	Glu	Leu	His	Asp	Asn	Asn	155	160	165
Val	Arg	Ser	Val	Ile	Arg	Gly	Ser	Asp	Val	Asn	His	Asp	Gly	Ala	170	175	180
Lys	Asp	Gly	Ile	Thr	Met	Pro	Asn	Ser	Lys	Ala	Gln	Glu	Ser	Leu	185	190	195
Ile	Arg	Lys	Thr	Tyr	Lys	Asn	Ala	Gly	Leu	Ser	Thr	Asn	Asp	Thr	200	205	210

Gln Tyr Phe Glu

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

TATTTTATTG GAGACAACAT ACGAAGCACT TGAAAATAGT GAGTAAGCCA 50
TGACCGTATT AAGTAAAAGC TCACGAACAG TAAAGGTGGC ACCCCTCTGG 100
CTAGCATTTC CGGCCAAAAT GTAGGCGTTT ACGTTGGTGC ATCCATGTCA 150
GACTACAACG AGCTTTTCGC AAAGGACCCG GATACCAATT TGACATATCG 200
TATTACCGGA ACTGCATCAA ATATTTTGTG AAATCGACTC TCCTACATGT 250
TCGACCTTCA CGGGCCAAGT TTCACGGTGG ACGTGCCTG CTCATCAAGC 300
TTGGCCGCAT TCCATCTGGC CTGTCTAGAG TTGAAGACGG GAGAGGTCCG 350
GCAAGCCATC GTGGGCGGGG CTTACCTTGT ATTATCCCCA GATCCTACGA 400
TCGGAATGAG CAAACTCAGG CTTTACGGCG AACATGGTCG CTCATACACT 450
TACGATCACC GAGGGACTGG ATACGGTCGT GCGGAGGGCG TCGCTAGCCT 500
AATTCTTAAG CCTTTACAAG ATGCTATCGA CGTGGGTGAT ACAATTTCGAG 550
CAATCATACG TAACACTGGA ATGAATCAAG ACGGGAAGAC GAACGGAATT 600
ACGCTCCCAA GCAAAGACGC CCAAGAAAGC CTCATAAGGT CTGTCTACAC 650
AGCTGCAGGT CTCGATCCAC TGTATACTTC CTACGTTGAG 690

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Ile Leu Leu Glu Thr Thr Tyr Glu Ala Leu Glu Asn Ser Gly Thr
      5                      10                      15

Pro Leu Ala Ser Ile Arg Gly Gln Asn Val Gly Val Tyr Val Gly
      20                      25                      30

Ala Ser Met Ser Asp Tyr Asn Glu Leu Phe Ala Lys Asp Pro Asp
      35                      40                      45

Thr Asn Leu Thr Tyr Arg Ile Thr Gly Thr Ala Ser Asn Ile Leu
      50                      55                      60

Ser Asn Arg Leu Ser Tyr Met Phe Asp Leu His Gly Pro Ser Phe
      65                      70                      75

Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Ala Ala Phe His Leu
      80                      85                      90

Ala Cys Gln Ser Leu Lys Thr Gly Glu Val Arg Gln Ala Ile Val
      95                      100                     105

Gly Gly Ala Tyr Leu Val Leu Ser Pro Asp Pro Thr Ile Gly Met
      110                     115                     120

Ser Lys Leu Arg Leu Tyr Gly Glu His Gly Arg Ser Tyr Thr Tyr

```

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	125		130		135
Asp His Arg Gly Thr Gly Tyr Gly Arg Gly Glu Gly Val Ala Ser					
	140		145		150
Leu Ile Leu Lys Pro Leu Gln Asp Ala Ile Asp Val Gly Asp Thr					
	155		160		165
Ile Arg Ala Ile Ile Arg Asn Thr Gly Met Asn Gln Asp Gly Lys					
	170		175		180
Thr Asn Gly Ile Thr Leu Pro Ser Lys Asp Ala Gln Glu Ser Leu					
	185		190		195
Ile Arg Ser Val Tyr Thr Ala Ala Gly Leu Asp Pro Leu Tyr Thr					
	200		205		210
Ser Tyr Val Glu					

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

GCGAATGCTA GAGACGGCTT ATCACGCTCT GGAGGACGGT AAGTCTAACC 50
AGTGCAAATT TAGGGGCTAT AATCTTGGTG TGTGAGAATA ACATACCATC 100
AGCGAGCATC CCCCTGGAGA AGTGCTTCGG CTCAGACACT TCCGTTTATA 150
CCGGTGCTT CACCAACGAT TATCTCAGCA TACTGCAGCA AGACTTTGAG 200
GCTGAGCAAA GGCACGCAGC CATGGGAATC GCGCCCTCCA TGTTGGCCAA 250
TCGCCAAGC TGGTTCTTCA ACTTCAAGGG GACATCGATG AACCTGGATT 300
CGGCCTGCTC CAGCAGTCTG GTTGCACTGC ATCTTGCTTC ACAGGACCTC 350
CGTGCTGGTA CCACATCGAT GGTATGTATC GATCATAAAA TCACGTACTC 400
CTTCATTAAT AAATAAATGT TTTAGGCACT AGTTGGAGGG GCGAATCTTG 450
TCTACCACCC CGACTTCATG GAGATGATGT CAAACTTCAA CTTCTGTCT 500
CCCGACAGCC GTTCTTGAG TTTGATCAA CGTGCTAATG GTTATGCGCG 550
TGGGGAAGGA ACCGCCGTGA TGGTCGTCAA ACGCCTTGCA GATGCACTGC 600
GAGATGGAGA TACAATCAGA ACCGTAATCT GGAGTACCGG GTCGAACCAA 650
GACGGGAGAA CACCTGGGAT CACGCAGCCA AGTAAAGAAG CGCAGTTAAA 700
TCTCATCGAG CGCACCTACA AACAAGCGAA GATTGATATG GAGCCTACCA 750
GATTCTTCGA G

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

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(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg	Met	Leu	Glu	Thr	Ala	Tyr	His	Ala	Leu	Glu	Asp	Ala	Ser	Ile	5	10	15
Pro	Leu	Glu	Lys	Cys	Phe	Gly	Ser	Asp	Thr	Ser	Val	Tyr	Thr	Gly	20	25	30
Cys	Phe	Thr	Asn	Asp	Tyr	Leu	Ser	Ile	Leu	Gln	Gln	Asp	Phe	Glu	35	40	45
Ala	Glu	Gln	Arg	His	Ala	Ala	Met	Gly	Ile	Ala	Pro	Ser	Met	Leu	50	55	60
Ala	Asn	Arg	Leu	Ser	Trp	Phe	Phe	Asn	Phe	Lys	Gly	Thr	Ser	Met	65	70	75
Asn	Leu	Asp	Ser	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ala	Leu	His	Leu	80	85	90
Ala	Ser	Gln	Asp	Leu	Arg	Ala	Gly	Thr	Thr	Ser	Met	Ala	Leu	Val	95	100	105
Gly	Gly	Ala	Asn	Leu	Val	Tyr	His	Pro	Asp	Phe	Met	Glu	Met	Met	110	115	120
Ser	Asn	Phe	Asn	Phe	Leu	Ser	Pro	Asp	Ser	Arg	Ser	Trp	Ser	Phe	125	130	135
Asp	Gln	Arg	Ala	Asn	Gly	Tyr	Ala	Arg	Gly	Glu	Gly	Thr	Ala	Val	140	145	150
Met	Val	Val	Lys	Arg	Leu	Ala	Asp	Ala	Leu	Arg	Asp	Gly	Asp	Thr	155	160	165
Ile	Arg	Thr	Val	Ile	Trp	Ser	Thr	Gly	Ser	Asn	Gln	Asp	Gly	Arg	170	175	180
Thr	Pro	Gly	Ile	Thr	Gln	Pro	Ser	Lys	Glu	Ala	Gln	Leu	Asn	Leu	185	190	195
Ile	Glu	Arg	Thr	Tyr	Lys	Gln	Ala	Lys	Ile	Asp	Met	Glu	Pro	Thr	200	205	210
Arg	Phe	Phe	Glu														

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1221

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

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(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

AAGGAGGGGC CGCCCGGGAG AAGAAGTTAT CGTGGGCGCC GATTCGGTCG 50
ACCGGCAGCA ATTGCAGCCA GATTGCCGCG AGGGCTTCCT CCATTCCCGG 100
CGCGGGCGCA ACGAATCCGG TGTACTCCAG ATGCCGTGCG GTCCGGGGGA 150
GAGCTGCCTG ATCCAGTTTG AGATTCTTGT TTAAAGGAAG TTCGGCCAGC 200
TTCTCTATGG CGGCGGGGAC CATGTGAGCG GGGAGCAGAG CCTTCATGTG 250
CTGGCGAATC GTTTCGTGG ACGCTCCGCC GACTGCATAC GCCGCGAGAT 300
ACTTCTCGCC GGGGATATCG TCTCGGACCA GCACAACGCC GTCCGTGACG 350
CCCGGGCAGC ACTGCAGCGC GGCCTGAATT TCGCCGAGTT CTATGCGATG 400
CCCGCGAAGC TTGATCTGGC CGTCGTTTCT GCCCAGAAAA TCGATGCGCC 450
CATCCGGCAG ATAGCGCGCG CGATCGCCCG TCGGTACAT ACGCGCGCCC 500
GGAAATGGGC TAAACGGGTT CGGCACAAAG TAGGCTGCGG TGAGATCGCT 550
GCGCCCCGCA TAGCCGCGCG CGACACCGTC TCCGCGCAGC TACAGCCAGC 600
CTTCCACTCC CGGCGGAACG GGAGCGAATT GCTCGTCGAG CACGTAGGTT 650
TGGACGTTTC AAATTGGACG GCCGATGGGA ATCGACGGGG TCCCGGCGGG 700
GACCGAATCG ATGACGCCAC ACGCCGTGAG CATCGTGTTT TCGGTAGGGC 750
CGTAACCGTT CAAGAGCGCG GCGGGCTTGC CGTGCTCGAT CACCATGCGC 800
ATCCAGTGGG GATCCAGCGC TTCGCCCGCG ACAATCACAT TGGTCAGCGA 850
TTCGAATCCG GCTGGATCTT CGCGGGCAAC CTGATTGAAC AGAGATGCAG 900
TAAGGATAAT CGTGTCCACG TGGAAGCGGC GAAAGGCGAG AATCAGCTCG 1000
CGGGGCGCCA TCAAGGTCTC TTTCGAAAGA ACGACGATTC GCGCGCCATG 1050
CAGCAGGCCG CCCATAACT CGAAGGTGGG AGGGTCGAAA CCGAAGGCCG 1100
ACATCTGTCC CACGGTATCG GCGGGTGAGA ATTGTACGTA GTTGGTCCGG 1150
CTAACGAGGT TGACAATCGC CCCGTGGGGG ACGGCGACCC CCTTGGGCTT 1200
GCCGGTCGTG CCGGACGTGT A 1221

```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Tyr Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Val Ala Val Pro
      5                      10                      15

His Gly Ala Ile Val Asn Leu Val Ser Arg Thr Asn Tyr Val Gln
      20                      25                      30

Phe Ser Pro Ala Asp Thr Val Gly Gln Met Ser Ala Phe Gly Phe
      35                      40                      45

Asp Pro Pro Thr Phe Glu Leu Trp Gly Gly Leu Leu His Gly Ala
      50                      55                      60

Arg Ile Val Val Leu Ser Lys Glu Thr Leu Met Ala Pro Arg Glu
      65                      70                      75

Leu Ile Leu Ala Phe Arg Arg Phe His Val Asp Thr Ile Ile Leu
      80                      85                      90

```


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Thr	Ala	Ser	Leu	Phe	Asn	Gln	Val	Ala	Arg	Glu	Asp	Pro	Ala	Gly	95	100	105
Phe	Glu	Ser	Leu	Thr	Asn	Val	Ile	Val	Gly	Gly	Glu	Ala	Leu	Asp	110	115	120
Pro	His	Trp	Met	Arg	Met	Val	Ile	Glu	His	Gly	Lys	Pro	Ala	Arg	125	130	135
Leu	Leu	Asn	Gly	Tyr	Gly	Pro	Thr	Glu	Asn	Thr	Met	Leu	Thr	Ala	140	145	150
Cys	Gly	Val	Ile	Asp	Ser	Val	Pro	Ala	Gly	Thr	Pro	Ser	Ile	Pro	155	160	165
Ile	Gly	Arg	Pro	Ile	Ser	Asn	Val	Gln	Thr	Tyr	Val	Leu	Asp	Glu	170	175	180
Gln	Phe	Ala	Pro	Val	Pro	Pro	Gly	Val	Glu	Gly	Trp	Leu	Tyr	Ala	185	190	195
Ala	Gly	Asp	Gly	Val	Ala	Arg	Gly	Tyr	Ala	Gly	Arg	Ser	Asp	Leu	200	205	210
Thr	Ala	Ala	Tyr	Phe	Val	Pro	Asn	Pro	Phe	Ser	Pro	Phe	Pro	Gly	215	220	225
Ala	Arg	Met	Tyr	Arg	Thr	Gly	Asp	Arg	Ala	Arg	Tyr	Leu	Pro	Asp	230	235	240
Gly	Arg	Ile	Asp	Phe	Leu	Gly	Arg	Asn	Asp	Gly	Gln	Ile	Lys	Leu	245	250	255
Arg	Gly	His	Arg	Ile	Glu	Leu	Gly	Glu	Ile	Gln	Ala	Ala	Leu	Gln	260	265	270
Ser	Cys	Pro	Gly	Val	Thr	Asp	Gly	Val	Val	Leu	Val	Arg	Asp	Asp	275	288	285
Ile	Pro	Gly	Glu	Lys	Tyr	Leu	Ala	Ala	Tyr	Ala	Val	Gly	Gly	Ala	290	295	300
Ser	Thr	Glu	Thr	Ile	Arg	Gln	His	Met	Lys	Ala	Leu	Leu	Pro	Ala	305	310	315
His	Met	Val	Pro	Ala	Ala	Ile	Glu	Lys	Leu	Ala	Glu	Leu	Pro	Leu	320	325	330
Asn	Lys	Asn	Leu	Lys	Leu	Asp	Gln	Ala	Ala	Leu	Pro	Arg	Thr	Ala	335	340	345
Arg	His	Leu	Glu	Tyr	Thr	Gly	Phe	Val	Ala	Pro	Ala	Pro	Gly	Met	350	355	360
Glu	Glu	Ala	Leu	Ala	Ala	Ile	Trp	Leu	Gln	Leu	Leu	Pro	Val	Asp			

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	365		370		375
Arg Ile Gly Ala His Asp Asn Phe Phe Ser Arg Ala Ala Pro Pro					
	380		385		390

(2) INFORMATION FOR SEQ ID NO:83

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1222

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

CGTTTCACCC CAAGAATCTC AGACCATATA TCAGCAATGG CCTTCTCCCT 50
GGCATTGCCG GGAGCGACAT AGATCGGATC CCGAATCACA GTATCGCGAT 100
CAAATGGCGG CAGGGCGTTT CGGTCAATCT TGCCGTTTCGG CGTTAAAGGG 150
AGAGAATCGA CAATGACGAA GGCGCTGGGC ACCATGTAGT CCGGCAGTTT 200
TGCCTTCAGA TGGGCGCGCA ATTCGCTTAT TTCGGGAGCA CCTTCCCGTG 250
CGACGATATA AGCAACTAAT TGCTTTTCTT CGCTAGGGTC TTTTGTTCGTT 300
GTGACCACAG CTTCTCGAAT CGGGGATGTT GCGCAACAGG ACTTCGATTT 350
CTCCAGCTCG ATGCGATAGC CGCGAATCTT GACCTGATTG TCGGTGCGGC 400
CGATAAACTC GATGTTGCCA TCCGGCAAAT AACGCGCAAG ATCGCCAGTT 450
CGATAGAGGC GCTGCGCTGG CTCGCGATCG AATGAATGGT AGATGAACCT 500
CTCCGCCGTC AGTTCCGGCC GGTGAGATA CCCTCGCGCC AGTCCGTCGC 550
CGCCAATGTA GATCTCTCCA ACCACGCCGA TCGGCACCGG ATTGAGATGA 600
GCATCCAGTA TGTAGATCTG CGTATTCGCG ATCGGTCGGC CAATGGGCGG 650
TAATTCTCCC CAGCACTCTG GCGGACCGTC CACAGTAAAC GCTGTCACAA 700
CGTGGCTTTC CGTCGGCCCA TACTGGTTGA CCAAATGACA CTCGGGCAAC 750
GTGTCAAGGA AACTTCTGAT CCGCGGCGTT ATCTGCAGCC GCTCTCCCGC 800
CGTAATGACT TCGCGCAGCT GCGGCAAAAC CACATTCTCC ATGTGCGCGG 850
CTTCCGCCAT CTGTTGCAGT ACGACAAAAG GCACAAAAAG TCTCTCTACT 900
CGCTTCATTC GCAGGAAATT CAACAGGGCT GCGGATCGC GTCGGATTTG 950
CGCGGGCAGT AGCACCAGTG TGCCTCCTGA GCACCACGTG CTAAACATCT 1000
CTTGAAACGA AACATCGAAA CTCAACGAGG CAAACTGTAA CGTTCGCGCC 1050
GGCACCGAAC GAGAAAAATC CTCAATTTGC CACGCGATCA GGTTGGCAAG 1100
CGCGCGGTGT TCCATACCA CACCTTTCGG CTTGCCCCGC GTGCCAATCC 1150
CGCGGCCATG GCGGCCGGA GCATGCGACG TCGGGCCCCA TTCGCCCTAT 1200
AGTGAGTCGT ATTACAATTC AA 1222

```

(2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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Gly	Thr	Thr	Gly	Lys	Pro	Lys	Gly	Val	Val	Met	Glu	His	Arg	Ala	5	10	15
Leu	Ala	Asn	Leu	Ile	Ala	Trp	Gln	Ile	Glu	Asp	Phe	Ser	Arg	Ser	20	25	30
Val	Pro	Ala	Arg	Thr	Leu	Gln	Phe	Ala	Ser	Leu	Ser	Phe	Asp	Val	35	40	45
Ser	Phe	Gln	Glu	Met	Phe	Ser	Thr	Trp	Cys	Ser	Gly	Gly	Thr	Leu	50	55	60
Val	Leu	Leu	Pro	Ala	Gln	Ile	Arg	Arg	Asp	Pro	Pro	Ala	Leu	Leu	65	70	75
Asn	Phe	Leu	Arg	Met	Lys	Arg	Val	Glu	Arg	Leu	Phe	Val	Pro	Phe	80	85	90
Val	Val	Leu	Gln	Gln	Met	Ala	Glu	Ala	Ala	His	Met	Glu	Asn	Val	95	100	105
Val	Leu	Pro	Gln	Leu	Arg	Glu	Val	Ile	Thr	Ala	Gly	Glu	Arg	Leu	110	115	120
Gln	Ile	Thr	Pro	Arg	Ile	Arg	Ser	Phe	Leu	Asp	Thr	Leu	Pro	Glu	125	130	135
Cys	His	Leu	Val	Asn	Gln	Tyr	Gly	Pro	Thr	Glu	Ser	His	Val	Val	140	145	150
Thr	Ala	Phe	Thr	Val	Asp	Gly	Pro	Pro	Glu	Cys	Trp	Gly	Glu	Leu	155	160	165
Pro	Pro	Ile	Gly	Arg	Pro	Ile	Ala	Asn	Thr	Gln	Ile	Tyr	Ile	Leu	170	175	180
Asp	Ala	His	Leu	Asn	Pro	Val	Pro	Ile	Gly	Val	Val	Gly	Glu	Ile	185	190	195
Tyr	Ile	Gly	Gly	Asp	Gly	Leu	Ala	Arg	Gly	Tyr	Leu	Asn	Arg	Pro	200	205	210
Glu	Leu	Thr	Ala	Glu	Arg	Phe	Ile	Tyr	His	Ser	Phe	Asp	Arg	Glu	215	220	225
Pro	Ala	Gln	Arg	Leu	Tyr	Arg	Thr	Gly	Asp	Leu	Ala	Arg	Tyr	Leu	230	235	240
Pro	Asp	Gly	Asn	Ile	Glu	Phe	Ile	Gly	Arg	Thr	Asp	Asn	Gln	Val	245	250	255
Lys	Ile	Arg	Gly	Tyr	Arg	Ile	Glu	Leu	Glu	Lys	Ser	Lys	Ser	Cys	260	265	270
Cys	Ala	Thr	Ser	Pro	Ile	Arg	Glu	Ala	Val	Val	Thr	Thr	Thr	Lys			

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	275		288		285
Asp Pro Ser Glu	Glu Lys Gln Leu Val	Ala Tyr Ile Val Ala	Arg		
	290	295	300		
Glu Gly Ala Pro	Glu Ile Ser Glu Leu	Arg Ala His Leu Lys	Ala		
	305	310	315		
Lys Leu Pro Asp	Tyr Met Val Pro Ser	Ala Phe Val Ile Val	Asp		
	320	325	330		
Ser Leu Pro Leu	Thr Pro Asn Gly Lys	Ile Asp Arg Asn Ala	Leu		
	335	340	345		
Pro Pro Phe Asp	Arg Asp Thr Val Ile	Arg Asp Pro Ile Tyr	Val		
	350	355	360		
Ala Pro Gly Asn	Ala Arg Glu Lys Ala	Ile Ala Asp Ile Trp	Ser		
	365	370	375		
Glu Ile Leu Gly	Val Lys Arg Ile Gly	Val His Asp Asn Phe	Phe		
	380	385	390		
Ala Pro Gly Gly	Pro Ser				
	395				

(2) INFORMATION FOR SEQ ID NO:85

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1200

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

AATCTACACG TCCGGCACCA CCGGCAAGCC CAAGGGGGCC ATAATCCATC 50
ACCTGGGACT GGC GAATTAC TTGGTGTGGT GCTCGCGGGC TTACGCGATT 100
GCTCAAGGAG TGGGAGCACC GGTCCACTCG TCGATCTCGT TCGATCTGAC 150
GATCACTGCC TTGCTTGCCC CCTTGGTCGT CGGCCGGCGC ATCGACCTGC 200
TTGATGAAGA ACTGGGCATC GAGCAACTGA GTTACGCTCT CCGGCGATCG 250
CGCGACTATA GCCTGGTCAA GATCACTCCG GCTCACCTGC GCTGGCTCGG 300
CGATGAACTG GGACCCTGCG AGGCCGAAGG TCGTACGCGA GCTTTTCATCA 350
TCGGTGGTGA GCAACTGACG GCCGAACACG TCKCATTCTG GAGGCGGCAC 400
GCGCCGGGGA CGAGCCTGAT CAACGAGTAT GGTCCGACCG AGACGGTCGT 450
CGGCTGCTGC GTGTACCGCG TGCCTCCTGA CCAGGAGATT TCGGGGCCCCA 500
TCCCGATTGG CCGACCGATC GCCAACACGC GTCTCTACGT CCTCGATCCG 550
GATCTCGCGC TGGTACCCAT CGGCGTTGCA GGCGAGCTGT ACATCGGCGG 600
TGCCGGGGGT GCGCGGGGGT ATCTCAACAG GCCCGGCCTG ACCGCTGAAA 650
GGTTCATCCC CGACCCGTTT GGCAAGAAGC CGGGCGAGCG CCTCTATCGC 700
ACCGGAGACC TCGCCCGATG GCGGTCCGAC GGTAACCTCG AGTATCTCGG 750
CAGGGTCGAT CGCCAGGTTA AAGTCCGCGG GTTTCGGATC GAACCCGGGG 800
AGATCGAACA GGC ACTCGCC CGGCACTCCG CGGTACGCGA GTCCGTCGTG 850
GTCGCAAGCG CAGGTGCATC GGACGTGCAA CGCCTCGTCG CCTATCTGGT 900

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TCTTGCGGAG GCAGGGCCGG CACCGCCCGA CTCGGAGCTG CGCGAGTTCC 950
 TGCGGACGTT ACTCCCCGAG CCGATGATAC CCTCGGCATT CGTTGTGCTG 1000
 GAGACGCTCC CACTGACCCA CAACGGGAAG GTGGACCGAG AGGCCCTGCC 1050
 GGCCCCTGAG GGTGTGCCCT TCCGTGGGGA TGCTCGTTTC GTTGCTCCCC 1100
 GCGGCCCGCT CGAACAGGAG GTGGCATCGA TCTGGGGTGC AGTCCTCGGA 1150
 CTGGAGCGTA TCGGCGCCCT TGACAACTTC TTCTTCCCTC GGCGGCCCT 1200

(2) INFORMATION FOR SEQ ID NO:86

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ile	Tyr	Thr	Ser	Gly	Thr	Thr	Gly	Lys	Pro	Lys	Gly	Ala	Ile	Ile	5	10	15
His	His	Leu	Gly	Leu	Ala	Asn	Tyr	Leu	Val	Trp	Cys	Ser	Arg	Ala	20	25	30
Tyr	Ala	Ile	Ala	Gln	Gly	Val	Gly	Ala	Pro	Val	His	Ser	Ser	Ile	35	40	45
Ser	Phe	Asp	Leu	Thr	Ile	Thr	Ala	Leu	Leu	Ala	Pro	Leu	Val	Val	50	55	60
Gly	Arg	Arg	Ile	Asp	Leu	Leu	Asp	Glu	Glu	Leu	Gly	Ile	Glu	Gln	65	70	75
Leu	Ser	Tyr	Ala	Leu	Arg	Arg	Ser	Arg	Asp	Tyr	Ser	Leu	Val	Lys	80	85	90
Ile	Thr	Pro	Ala	His	Leu	Arg	Trp	Leu	Gly	Asp	Glu	Leu	Gly	Pro	95	100	105
Cys	Glu	Ala	Glu	Gly	Arg	Thr	Arg	Ala	Phe	Ile	Ile	Gly	Gly	Glu	110	115	120
Gln	Leu	Thr	Ala	Glu	His	Val	Xaa	Phe	Trp	Arg	Arg	His	Ala	Pro	125	130	135
Gly	Thr	Ser	Leu	Ile	Asn	Glu	Tyr	Gly	Pro	Thr	Glu	Thr	Val	Val	140	145	150
Gly	Cys	Cys	Val	Tyr	Arg	Val	Pro	Pro	Asp	Gln	Glu	Ile	Ser	Gly	155	160	165
Pro	Ile	Pro	Ile	Gly	Arg	Pro	Ile	Ala	Asn	Thr	Arg	Leu	Tyr	Val	170	175	180
Leu	Asp	Pro	Asp	Leu	Ala	Leu	Val	Pro	Ile	Gly	Val	Ala	Gly	Glu	185	190	195

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Leu	Tyr	Ile	Gly	Gly	Ala	Gly	Val	Ala	Arg	Gly	Tyr	Leu	Asn	Arg
				200					205					210
Pro	Gly	Leu	Thr	Ala	Glu	Arg	Phe	Ile	Pro	Asp	Pro	Phe	Gly	Lys
				215					220					225
Lys	Pro	Gly	Glu	Arg	Leu	Tyr	Arg	Thr	Gly	Asp	Leu	Ala	Arg	Trp
				230					235					240
Arg	Ser	Asp	Gly	Asn	Leu	Glu	Tyr	Leu	Gly	Arg	Val	Asp	Arg	Gln
				245					250					255
Val	Lys	Val	Arg	Gly	Phe	Arg	Ile	Glu	Pro	Gly	Glu	Ile	Glu	Gln
				260					265					270
Ala	Leu	Ala	Arg	His	Ser	Ala	Val	Arg	Glu	Ser	Val	Val	Val	Ala
				275					288					285
Ser	Ala	Gly	Ala	Ser	Asp	Val	Gln	Arg	Leu	Val	Ala	Tyr	Leu	Val
				290					295					300
Leu	Ala	Glu	Ala	Gly	Pro	Ala	Pro	Pro	Asp	Ser	Glu	Leu	Arg	Glu
				305					310					315
Phe	Leu	Arg	Thr	Leu	Leu	Pro	Glu	Pro	Met	Ile	Pro	Ser	Ala	Phe
				320					325					330
Val	Val	Leu	Glu	Thr	Leu	Pro	Leu	Thr	His	Asn	Gly	Lys	Val	Asp
				335					340					345
Arg	Glu	Ala	Leu	Pro	Ala	Pro	Glu	Gly	Val	Pro	Phe	Arg	Gly	Asp
				350					355					360
Ala	Arg	Phe	Val	Ala	Pro	Arg	Gly	Pro	Leu	Glu	Gln	Glu	Val	Ala
				365					370					375
Ser	Ile	Trp	Gly	Ala	Val	Leu	Gly	Leu	Glu	Arg	Ile	Gly	Ala	Leu
				380					385					390
Asp	Asn	Phe	Phe	Phe	Pro	Arg	Arg	Pro						
				395										

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1204

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGGGGCCCGCC GGGCGAGAAG AAGTTCGCGG TGATGCTCAC CGGCGCGTCG 50
 AGCTTCAACG CTCCTGCCA GATCTCCGCG AGCTTGCTCT CCGTCTCCGT 100

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```

GCCCCGGCGCT ACGTATTGGG CGCCGGCGCT ACGGTCGATG GACGGCAGCG 150
CCTTACGATC GATCTTGCCG TTGGCATTCA GCGGAAAGGC CTCCAGGACG 200
CGCCAGCCGC TGGGAATCAT GTACTCGGGC AGGGCCAGCT TGAGGCGCAT 250
CCGCAGCGCC GAGATGAGCA CCTCTTCGTC CGCGGTCTGG GCCACGACGT 300
AGGCGACGAG GGCCTTGTTT TCCCCCTCTC CCTGCGCCAC GACCAGGGCG 350
TCGTCGACGC CAGCCTCGGT CTTACAGCGC GTCTCGATCT CGCCGAGCTC 400
GATGCGGAAG CCGCGGATCT TGATCTGGTC GTCGAGGCGG CCGAGGAACT 450
CGAGATCGCC GCTGGCGAGC CGGCGAACGA GGTCGCCGCT GCGATAGAGG 500
CGCCCTTCGC CGAAGGGATT GGCGATGAAC TTCGCCGCCG TCAGCTCCGG 550
CTGGTTGACG TAGCCTCTGG CCACCCCTGC CCCGCCAATG CACAGCTCCG 600
CGGCCACGCC GACCGGCGCG ATCTCCAGTG CCTCGTTGAG GACATACAGC 650
TCCGTGTTGT CCATGGCCCT GCCGATGGGC AGGCGCTCCG GCAGGCCGGC 700
CTGGAGAGCG GCGGTGACGT CGAACATGGC GCAGCCGACC ACGGTCTCCG 750
TGGGACCGTA GTGGTTGTAG ATCTGGGCGT GGGGGAAGCG CGTTTGCAGC 800
TCGCGGGCGA GCGAGGCGGG AAACGATTCT CCGCCGATGA CGAAAACGTG 850
TTGAGATGAA GCCCGGGCCG TGTCTCCGT CAGCTCCGCG CTGTCGAGCA 900
GAGCGAGCAT ACCGGTGAGA TGCATCGGCG TCATGCGCAG CAGATAAGCC 950
CGTTCGTCGC CGGCCAACGC TTTGCGGAGC TCGTTCAACT CATCGCCGGG 1000
CGTGGTCAGC GAGACGCAGC CACCCCGGAG CAAGGGAACA TACAGGCTGG 1050
GCACGGTGAT GTCGAAGCCG TGGGAGGTGA CGACGAGGGA GCCGGCCAAC 1100
CCCTTCGCGT AGTAGCGCTG CGAAGCGAAG GCGCAGTAGT CACTGAGGCC 1150
GGCGTGTCTG ATCTCCACGC CCTTCGGCTT GCCCGTCGTG CCGGACGTGT 1200
AGAT 1204

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Ile Tyr Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Val Glu Ile
      5                      10                      15
Arg His Ala Gly Leu Ser Asp Tyr Cys Ala Phe Ala Ser Gln Arg
      20                      25                      30
Tyr Tyr Ala Lys Gly Leu Ala Gly Ser Leu Val Val Thr Ser His
      35                      40                      45
Gly Phe Asp Ile Thr Val Pro Ser Leu Tyr Val Pro Leu Leu Arg
      50                      55                      60
Gly Gly Cys Val Ser Leu Thr Thr Pro Gly Asp Glu Leu Asn Glu
      65                      70                      75
Leu Ala Lys Ala Leu Ala Gly Asp Glu Arg Ala Tyr Leu Leu Arg
      80                      85                      90
Met Thr Pro Met His Leu Thr Gly Met Leu Ala Leu Leu Asp Ser
      95                      100                     105

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Ala	Glu	Leu	Thr	Glu	Asp	Thr	Ala	Arg	Ala	Ser	Ser	Gln	His	Val
				110					115					120
Phe	Val	Ile	Gly	Gly	Glu	Ser	Phe	Pro	Ala	Ser	Leu	Ala	Arg	Glu
				125					130					135
Leu	Gln	Thr	Arg	Phe	Pro	His	Ala	Gln	Ile	Tyr	Asn	His	Tyr	Gly
				140					145					150
Pro	Thr	Glu	Thr	Val	Val	Gly	Cys	Ala	Met	Phe	Asp	Val	Thr	Ala
				155					160					165
Ala	Leu	Gln	Ala	Gly	Leu	Pro	Glu	Arg	Leu	Pro	Ile	Gly	Arg	Ala
				170					175					180
Met	Asp	Asn	Thr	Glu	Leu	Tyr	Val	Leu	Asn	Glu	Ala	Leu	Glu	Ile
				185					190					195
Ala	Pro	Val	Gly	Val	Ala	Gly	Glu	Leu	Cys	Ile	Gly	Gly	Ala	Gly
				200					205					210
Val	Ala	Arg	Gly	Tyr	Val	Asn	Gln	Pro	Glu	Leu	Thr	Ala	Ala	Lys
				215					220					225
Phe	Ile	Ala	Asn	Pro	Phe	Gly	Glu	Gly	Arg	Leu	Tyr	Arg	Ser	Gly
				230					235					240
Asp	Leu	Val	Arg	Arg	Leu	Ala	Ser	Gly	Asp	Leu	Glu	Phe	Leu	Gly
				245					250					255
Arg	Leu	Asp	Asp	Gln	Ile	Lys	Ile	Arg	Gly	Phe	Arg	Ile	Glu	Leu
				260					265					270
Gly	Glu	Ile	Glu	Thr	Ala	Leu	Lys	Thr	Glu	Ala	Gly	Val	Asp	Asp
				275					288					285
Ala	Leu	Val	Val	Ala	Gln	Gly	Glu	Gly	Glu	Asn	Lys	Ala	Leu	Val
				290					295					300
Ala	Tyr	Val	Val	Ala	Gln	Thr	Ala	Asp	Glu	Glu	Val	Leu	Ile	Ser
				305					310					315
Ala	Leu	Arg	Met	Arg	Leu	Lys	Leu	Ala	Leu	Pro	Glu	Tyr	Met	Ile
				320					325					330
Pro	Ser	Gly	Trp	Arg	Val	Leu	Glu	Ala	Phe	Pro	Leu	Asn	Ala	Asn
				335					340					345
Gly	Lys	Ile	Asp	Arg	Lys	Ala	Leu	Pro	Ser	Ile	Asp	Arg	Ser	Ala
				350					355					360
Gly	Ala	Gln	Tyr	Val	Ala	Pro	Gly	Thr	Glu	Thr	Glu	Ser	Lys	Leu
				365					370					375
Ala	Glu	Ile	Trp	Gln	Glu	Ala	Leu	Lys	Leu	Asp	Ala	Pro	Val	Ser

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	380		385		390
Ile Thr Ala Asn Phe Phe Ser Pro Gly Gly Pro					
	395		400		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1190

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATCTACACCT	CGGGCACGAC	CGGCAAGCCG	AAGGGGATCA	TGTATTTCGCA	50
TCGATACCTG	TTGCATAATA	TGCGCAACTA	CGGCGACTTA	TTTCAGGTCT	100
CCCCCACGA	TCGCTGGAGT	TGGTTGCATT	CCTACAGCTA	TGCTTCGGCG	150
AATACTGATA	TCCTTTGCCC	GCTACTGCAC	GGCGCCGCCG	TCTGCCCTTG	200
GAATTTGCAT	CGTAATGGCC	TATCGGGCTT	AGCTCGTTGG	CTCGCCGAGT	250
CGCGAATCAC	CATTTTGAAC	TGGATGCCGA	CACCGCTACG	CAGTTTGGCA	300
AAGCTCTGGC	CGCCAAAGCA	CGTGCTTCCC	GATCTGCGAC	TTACAGTGTT	350
GGGCGGCGAA	ACGCTGTTTG	CCCAAGACGT	TGCTGACTTT	CGGCGAATAA	400
TTTCGCTGAA	TTGCCTAATC	GCCAATCGTC	TGGGAACTTC	GGAAACTGGA	450
TTGTTTCGGC	TCGCGTTTCT	CGACCGAGAG	ACTCCCCTTG	CTAATGGTTC	500
CATACAGGCC	GGATACGAAG	TTCCAGACAA	GACCGTCGTC	CTGTTTCGACG	550
AATATGGAGT	TGAGCTGGCC	CCTGGCAACG	TCGGTCAGAT	TGGCGTGCGC	600
AGCAGGTA	TGCCGCCTGG	ATACTGGCGA	CGGCCGGAGT	TGACAAGCGA	650
GCGATTTCTA	ACCAGTAAAG	GCGATGATGA	CGTACGGACC	TTCCTCACCG	700
GCGACCTTGG	GCGAATGCGG	GACGACGGAT	GCCTCGAGCA	CTGCGGACGG	750
CTCGACTCCC	AAGTGAAGAT	CCGTGGTCAC	CGCATCGCAA	TGGGAGAGAT	800
CGAATTCTTG	CTTCGGACAT	GCGACGGAGT	CAGCGAAGCA	GTTGTTCATTG	850
CCAGGCCACA	TTCAGACGGT	GAAACCCGTT	TGATAGCTTA	TTTTGTGCCG	900
ACCGAGAAAA	GCGCTATCGA	TGTATCGAGC	CTTCGTCGGC	ACCTGCTGGG	950
AAAGCTGCCT	GGCCACATGA	TCCCCTCGGC	GTTTGTGCGG	CTCGACGGCG	1000
TGCCCCAAAA	CGCCAACCAA	AAAGTAGATT	GGGCGGCCTT	GCCAGCACCG	1050
AACTTCCAAA	ACCAGGGACA	GCAGCACGTA	CCGCCACAAA	CGCCTTGGCA	1100
GCGACATCTC	GTGGAGTTGT	GGCAAAAGTT	GTTGAATGTG	GAATCGATCG	1150
GCATCCACGA	TGACTTCTTC	GCCCTCGGCG	GCCCCCTCCTT		1190

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ile Tyr Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Ile Met Tyr														
	5						10						15	

Ser His Arg Tyr Leu Leu His Asn Met Arg Asn Tyr Gly Asp Leu

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20										25					30				
Phe	Gln	Val	Ser	Pro	His	Asp	Arg	Trp	Ser	Trp	Leu	His	Ser	Tyr					
				35					40					45					
Ser	Tyr	Ala	Ser	Ala	Asn	Thr	Asp	Ile	Leu	Cys	Pro	Leu	Leu	His					
				50					55					60					
Gly	Ala	Ala	Val	Cys	Pro	Trp	Asn	Leu	His	Arg	Asn	Gly	Leu	Ser					
				65					70					75					
Gly	Leu	Ala	Arg	Trp	Leu	Ala	Glu	Ser	Arg	Ile	Thr	Ile	Leu	Asn					
				80					85					90					
Trp	Met	Pro	Thr	Pro	Leu	Arg	Ser	Leu	Ala	Lys	Leu	Trp	Pro	Pro					
				95					100					105					
Lys	His	Val	Leu	Pro	Asp	Leu	Arg	Leu	Thr	Val	Leu	Gly	Gly	Glu					
				110					115					120					
Thr	Leu	Phe	Ala	Gln	Asp	Val	Ala	Asp	Phe	Arg	Arg	Ile	Ile	Ser					
				125					130					135					
Leu	Asn	Cys	Leu	Ile	Ala	Asn	Arg	Leu	Gly	Thr	Ser	Glu	Thr	Gly					
				140					145					150					
Leu	Phe	Arg	Leu	Ala	Phe	Leu	Asp	Arg	Glu	Thr	Pro	Leu	Ala	Asn					
				155					160					165					
Gly	Ser	Ile	Gln	Ala	Gly	Tyr	Glu	Val	Pro	Asp	Lys	Thr	Val	Val					
				170					175					180					
Leu	Phe	Asp	Glu	Tyr	Gly	Val	Glu	Leu	Ala	Pro	Gly	Asn	Val	Gly					
				185					190					195					
Gln	Ile	Gly	Val	Arg	Ser	Arg	Tyr	Leu	Pro	Pro	Gly	Tyr	Trp	Arg					
				200					205					210					
Arg	Pro	Glu	Leu	Thr	Ser	Glu	Arg	Phe	Leu	Thr	Ser	Lys	Gly	Asp					
				215					220					225					
Asp	Asp	Val	Arg	Thr	Phe	Leu	Thr	Gly	Asp	Leu	Gly	Arg	Met	Arg					
				230					235					240					
Asp	Asp	Gly	Cys	Leu	Glu	His	Cys	Gly	Arg	Leu	Asp	Ser	Gln	Val					
				245					250					255					
Lys	Ile	Arg	Gly	His	Arg	Ile	Ala	Met	Gly	Glu	Ile	Glu	Phe	Leu					
				260					265					270					
Leu	Arg	Thr	Cys	Asp	Gly	Val	Ser	Glu	Ala	Val	Val	Ile	Ala	Arg					
				275					288					285					
Pro	His	Ser	Asp	Gly	Glu	Thr	Arg	Leu	Ile	Ala	Tyr	Phe	Val	Pro					
				290					295					300					

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Thr	Glu	Lys	Ser	Ala	Ile	Asp	Val	Ser	Ser	Leu	Arg	Arg	His	Leu
				305					310					315
Leu	Gly	Lys	Leu	Pro	Gly	His	Met	Ile	Pro	Ser	Ala	Phe	Val	Arg
				320					325					330
Leu	Asp	Gly	Val	Pro	Lys	Asn	Ala	Asn	Gln	Lys	Val	Asp	Trp	Ala
				335					340					345
Ala	Leu	Pro	Ala	Pro	Asn	Phe	Gln	Asn	Gln	Gly	Gln	Gln	His	Val
				350					355					360
Pro	Pro	Gln	Thr	Pro	Trp	Gln	Arg	His	Leu	Val	Glu	Leu	Trp	Gln
				365					370					375
Lys	Leu	Leu	Asn	Val	Glu	Ser	Ile	Gly	Ile	His	Asp	Asp	Phe	Phe
				380					385					390
Ala	Leu	Gly	Gly	Pro	Ser									
				395										

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AAGGAGGGGC	CGCCCGGCGC	GAAGAAGTTC	TCGTGTAGCC	CGACGCGTTC	50
CAGCTGCAGC	ACGGCGCACC	AGATCGCTGC	GACCTGCCGC	TGGACGTCCG	100
TCATGATCGC	GGTGTCGCT	GCGGCCGCTG	CCGCGCGATT	CACCTGTGGA	150
ATGGGCAGGG	CCTTGCGGTC	GATCTTGTCG	TTCGGCGTGA	GCGGCAGCGC	200
GGCGAGCGAT	ACGATCACCT	GTGGCACCAT	GTACTCGGGG	AGTCTCGCGC	250
GGAGCGCCGT	CCGGAGCTCG	TCGAGCGGCA	GCACGCCGTC	TTCTGCCGGG	300
ACGACGTACG	CCACCAGACG	CTGATCGCCG	GGGGTGTCCT	CGCGCACGAC	350
GGCCACGCTG	CGGCGCACCG	ACGGATGCTC	GGACAGGACC	GATTCTGATCT	400
CCCCCAGCTC	GATCCGGTAG	CCGCGAAGCT	TCACCTGATG	ATCTCGGCGT	450
CCGACGAACT	CGAGGGCCCG	ATCGGCGCGC	AGTCGTACGA	TGTCGCCGGT	500
GCGGTACACG	CGCTCCGCCG	GTCTGCCCGC	GACCTCGACG	ACGACGAACT	550
TTTCTGCCGT	GAGCTCGGGT	CGATGACGAT	AGCCCCGCGC	CACGCCCTCT	600
CCTCCGATGC	ACAGCTCACC	CGGCACGCCG	ATGGGAGCCT	GGCGACCCGC	650
GGCGTCGAGC	ACGTAGACGT	TCGTGTTGGC	GATGGGATGG	CCGATCGGAA	700
TATCGCGATC	GCAATCCGTG	ACCTGATGCA	CGGTCGACCA	GATCGTCGTC	750
TCGGTCGGGC	CGTACATGTT	CCACAGCGCC	CGCACCCCTG	ACGAGAGATC	800
GCGCGCGAGA	TCGCGTGGA	GGGCCTCCCC	GCCGCAGAGC	GCGGTGAGAT	850
CCGCTCTTGCC	TGCGCAGCCG	GCGTCGATGA	GCAGGCGCCA	GGTCGCGGGG	900
GTCGCCTGCA	TCATCGTCGC	TCTGCACGAT	TCGATGCGCT	CGCGAAGACG	950
CTCGCCGTCG	AGCACGTCGC	CGCGGGAGGC	GATGACCGTC	CTCCCGCCGA	1000
CGACGAGAGG	CAAGAACAGC	TCGAGACCCG	CGATGTCGAA	CGACGGCGTG	1050
GTGACCGCGA	GGAGCACGTC	GCCGGCTCGC	AAGCCTGGCT	CCTTCTGCAT	1100
GGCGCGCAGG	AAATTCACGA	GCTGGCGGTG	CTCGATCTCG	ACCCCTTTCG	1150

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GCTTGCCCGT CGTGCCCGAC GTGTAGAT

1178

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ile	Tyr	Thr	Ser	Gly	Thr	Thr	Gly	Lys	Pro	Lys	Gly	Val	Glu	Ile	5	10	15
Glu	His	Arg	Gln	Leu	Val	Asn	Phe	Leu	Arg	Ala	Met	Gln	Lys	Glu	20	25	30
Pro	Gly	Leu	Arg	Ala	Gly	Asp	Val	Leu	Leu	Ala	Val	Thr	Thr	Pro	35	40	45
Ser	Phe	Asp	Ile	Ala	Gly	Leu	Glu	Leu	Phe	Leu	Pro	Leu	Val	Val	50	55	60
Gly	Gly	Arg	Thr	Val	Ile	Ala	Ser	Arg	Gly	Asp	Val	Leu	Asp	Gly	65	70	75
Glu	Arg	Leu	Arg	Glu	Arg	Ile	Glu	Ser	Cys	Arg	Ala	Thr	Met	Met	80	85	90
Gln	Ala	Thr	Pro	Ala	Thr	Trp	Arg	Leu	Leu	Ile	Asp	Ala	Gly	Trp	95	100	105
Gln	Gly	Lys	Thr	Asp	Leu	Thr	Ala	Leu	Cys	Gly	Gly	Glu	Ala	Leu	110	115	120
Pro	Arg	Asp	Leu	Ala	Arg	Asp	Leu	Ser	Ser	Arg	Val	Arg	Ala	Leu	125	130	135
Trp	Asn	Met	Tyr	Gly	Pro	Thr	Glu	Thr	Thr	Ile	Trp	Ser	Thr	Val	140	145	150
His	Gln	Val	Thr	Asp	Cys	Asp	Arg	Asp	Ile	Pro	Ile	Gly	His	Pro	155	160	165
Ile	Ala	Asn	Thr	Asn	Val	Tyr	Val	Leu	Asp	Ala	Ala	Gly	Arg	Gln	170	175	180
Ala	Pro	Ile	Gly	Val	Pro	Gly	Glu	Leu	Cys	Ile	Gly	Gly	Glu	Gly	185	190	195
Val	Ala	Arg	Gly	Tyr	Arg	His	Arg	Pro	Glu	Leu	Thr	Ala	Glu	Lys	200	205	210

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Phe Val Val Val	Glu Val Ala Gly Arg	Pro Ala Glu Arg Val Tyr	
	215	220	225
Arg Thr Gly Asp	Ile Val Arg Leu Arg	Ala Asp Arg Ala Leu Glu	
	230	235	240
Phe Val Gly Arg	Arg Asp His Gln Val	Lys Leu Arg Gly Tyr Arg	
	245	250	255
Ile Glu Leu Gly	Glu Ile Glu Ser Val	Leu Ser Glu His Pro Ser	
	260	265	270
Val Arg Arg Ser	Val Ala Val Val Arg	Glu Asp Thr Pro Gly Asp	
	275	288	285
Gln Arg Leu Val	Ala Tyr Val Val Pro	Ala Glu Asp Gly Val Leu	
	290	295	300
Pro Leu Asp Glu	Leu Arg Thr Ala Leu	Arg Ala Arg Leu Pro Glu	
	305	310	315
Tyr Met Val Pro	Gln Val Ile Val Ser	Leu Ala Ala Leu Pro Leu	
	320	325	330
Thr Pro Asn Asp	Lys Ile Asp Arg Lys	Ala Leu Pro Ile Pro Gln	
	335	340	345
Val Asn Arg Ala	Ala Ala Ala Ala Ala	Asp Thr Ala Ile Met Thr	
	350	355	360
Asp Val Gln Arg	Gln Val Ala Ala Ile	Trp Cys Ala Val Leu Gln	
	365	370	375
Leu Glu Arg Val	Gly Leu His Glu Asn	Phe Phe Ala Pro Gly Gly	
	380	385	390
Pro Ser			

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATCTACACCT	CCGGCACGAC	GGGCAAGCCG	AAGGGAGTAA	AGATCACACA	50
TCGTGCCGTG	GTGAATTTTC	TGAACTCGAT	GCGGCGTGAA	CCAGGGCTGA	100
CCCCGGACGA	TGTGGTGCTC	TCGGTCACCA	CGCTGTCGTT	TGACATTGCC	150
GGACTCGAAC	TCCACCTGCC	CCTGACGACT	GGAGCCACGG	TCGTAGTGGC	200
GACCCAAGAC	GCGGTGTCCG	ACGCTGAACT	GCTGGTCAGA	GAGTTGGAGC	250

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GGACCGGAAC AACTCTGTTG CAGGCGACGC CAGTCACATG GCGAATGCTT 300
CTGGAGTCGG GCTGGAAAGG AAATCCGCGA CTCAAGGCTC TGGTCGGAGG 350
TGAGGCAGTG CCGAGGGGACC TGGTGAATCG GCTTGCTCCC CTTTGCGCGT 400
CACTTTGGAA CATGTACGGA CCAACGGAAA CCACGATCTG GTCAACGGTT 450
GGGCGTCTGG AGGCTGGAGA TGGTGTGTCT AGTATTGGCC GGCCCATCGA 500
CAATACGCGG ATTTACGTCG TGGATCCGTC GATACACCTT CAGCCCATCG 550
GAGTTCCCGG CGAATTGCTG ATTGGCGGAG AAGGATTGGC CGACGGATAT 600
CTGAAACGCG ATCAGTTGAC GGCAGAGAAG TTCATTCTCTG ATCCATTTGG 650
TGGGAGGCCT GGGTCTCGGC TGTATCGAAC CGGAGATCTT GCGCGCTGGC 700
GCGCGGACGG CACCTTGGAG TGTCTCGGAC GAATGGACCA ACAGGTGAAG 750
ATTCCGGGGTT CCCGGATCGA ATTGGGTGAG ATCGAAACCC TGTTGGCCTC 800
CCACCCGGAT GTGAAACAGA ACGTGGTGGT CGTACGCGAG GACAGCCCCG 850
GGGAAAAAAA ATTGGTGGGC TATTTCTGTC CGGCGAACGG ACGCAATCCC 900
GAAGTGATGG AATTTCTCAA ACATCTGCAG CGGACGCTTC CGGATTACAT 950
GGTCCCCTCA GTGTACGTGC CTTTGACCTC GGTTCGCTT ACACCAACG 1000
GAAAGATCGA CCGCAAGGCG CTGCCCCGAC CGGATATCAG CGCCGTCACG 1050
GTTTCCCGAG AGTCAATTGC GCCGCGCAAT CCCGCCGAAG AGCGGCTGGC 1100
AGCAATTTTC GCCAAGGTGC TTGGCACGCC GATCGCCTCG ATCCACGACA 1150
GCTTCTTCTC CCCGGGCGGC CCCTCCAT 1178

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(2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Ile Tyr Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Val Lys Ile
      5                               10                               15

Thr His Arg Ala Val Val Asn Phe Leu Asn Ser Met Arg Arg Glu
      20                               25                               30

Pro Gly Leu Thr Pro Asp Asp Val Val Leu Ser Val Thr Thr Leu
      35                               40                               45

Ser Phe Asp Ile Ala Gly Leu Glu Leu His Leu Pro Leu Thr Thr
      50                               55                               60

Gly Ala Thr Val Val Val Ala Thr Gln Asp Ala Val Ser Asp Ala
      65                               70                               75

Glu Leu Leu Val Arg Glu Leu Glu Arg Thr Gly Thr Thr Leu Leu
      80                               85                               90

Gln Ala Thr Pro Val Thr Trp Arg Met Leu Leu Glu Ser Gly Trp
      95                               100                              105

Lys Gly Asn Pro Arg Leu Lys Ala Leu Val Gly Gly Glu Ala Val
      110                              115                              120

Pro Arg Asp Leu Val Asn Arg Leu Ala Pro Leu Cys Ala Ser Leu

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				125					130					135
Trp	Asn	Met	Tyr	Gly	Pro	Thr	Glu	Thr	Thr	Ile	Trp	Ser	Thr	Val
				140					145					150
Gly	Arg	Leu	Glu	Ala	Gly	Asp	Gly	Val	Ser	Ser	Ile	Gly	Arg	Pro
				155					160					165
Ile	Asp	Asn	Thr	Arg	Ile	Tyr	Val	Val	Asp	Pro	Ser	Ile	His	Leu
				170					175					180
Gln	Pro	Ile	Gly	Val	Pro	Gly	Glu	Leu	Leu	Ile	Gly	Gly	Glu	Gly
				185					190					195
Leu	Ala	Asp	Gly	Tyr	Leu	Lys	Arg	Asp	Gln	Leu	Thr	Ala	Glu	Lys
				200					205					210
Phe	Ile	Pro	Asp	Pro	Phe	Gly	Gly	Arg	Pro	Gly	Ser	Arg	Leu	Tyr
				215					220					225
Thr	Gly	Asp	Leu	Ala	Arg	Trp	Arg	Ala	Asp	Gly	Thr	Leu	Glu	
				230					235					240
Cys	Leu	Gly	Arg	Met	Asp	Gln	Gln	Val	Lys	Ile	Arg	Gly	Ser	Arg
				245					250					255
Glu	Leu	Gly	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	His	Pro	Asp	
				260					265					270
Lys	Gln	Asn	Val	Val	Val	Val	Arg	Glu	Asp	Ser	Pro	Gly	Glu	
				275					288					285
Lys	Lys	Leu	Val	Gly	Tyr	Phe	Val	Pro	Ala	Asn	Gly	Arg	Asn	Pro
				290					295					300
Glu	Val	Met	Glu	Phe	Arg	Lys	His	Leu	Gln	Arg	Thr	Leu	Pro	Asp
				305					310					315
Tyr	Met	Val	Pro	Ser	Val	Tyr	Val	Pro	Leu	Thr	Ser	Val	Pro	Leu
				320					325					330
Thr	Pro	Asn	Gly	Lys	Ile	Asp	Arg	Lys	Ala	Leu	Pro	Ala	Pro	Asp
				335					340					345
Ile	Ser	Ala	Val	Thr	Val	Ser	Arg	Glu	Ser	Ile	Ala	Pro	Arg	Asn
				350					355					360
Pro	Ala	Glu	Glu	Arg	Leu	Ala	Ala	Ile	Phe	Ala	Lys	Val	Leu	Gly
				365					370					375
Thr	Pro	Ile	Ala	Ser	Ile	His	Asp	Ser	Phe	Phe	Ser	Pro	Gly	Gly
				380					385					390

Pro

CLAIMS

- 1 1. A method for recovery of antibiotic biosynthetic DNA from humic
2 materials or lichen comprising the steps of:
 - 3 (a) combining a humic or lichen-derived sample with a set of
4 amplification primers under conditions suitable for polymerase chain reaction amplification,
5 wherein the primer set is a degenerate primer set selected to hybridize with conserved regions
6 of antibiotic biosynthetic gene;
 - 7 (b) cycling the combined sample through a plurality of amplification
8 cycles to amplify DNA complementary to the primer set; and
 - 9 (c) isolating the amplified DNA.
- 1 2. The method according to claim 1, wherein the primer set hybridizes
2 with a polyketide synthase gene.
- 1 3. The method according to claim 2, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 1 and 2.
- 1 4. The method according to claim 2, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 3 and 4.
- 1 5. The method according to claim 2, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 5 and 6.
- 1 6. The method according to claim 2, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 11 and 12.
- 1 7. The method according to claim 1, wherein the primer set hybridizes
2 with a isopenicillin N synthase gene.

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1 8. The method according to claim 7, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 7 and 8.

1 9. The method according to claim 1, wherein the primer set hybridizes
2 with a peptide synthetase gene.

1 10. The method according to claim 9, wherein the primer set comprises
2 primers having the sequence set forth in SEQ ID Nos. 9 and 10.

1 11. The method according to any of claims 1 to 10, wherein the sample
2 comprises DNA extracted from a soil sample.

1 12. The method according to claim 1, wherein the sample is a lichen-
2 derived sample.

1 13. The method according to any of claims 1 to 12, further comprising the
2 steps of cloning the isolated DNA into a host organism, and isolating the cloned DNA.

1 14. The method according to claim 13, wherein the host organism is *E.*
2 *coli*.

1 15. An oligonucleotide primer having the sequence as defined in any of
2 Seq. ID. Nos. 1 through 8.

1 16. A composition comprising two oligonucleotide primers having the
2 sequence as defined in Seq. ID Nos. 1 and 2; 3 and 4; 5 and 6; or 7 and 8.

1 17. A polynucleotide comprising a region having the sequence given by
2 any of sequence ID Nos. 13, 15, 17, 19, 21, 23, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51,
3 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91 or 93.

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1 18. A biosynthetic polypeptide encoded by a polynucleotide comprising a
2 region having the sequence given by any of sequence ID Nos. 13, 15, 17, 19, 21, 23, 29, 31,
3 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 81,
4 83, 85, 87, 89, 91 or 93.

1 19. The biosynthetic polypeptide of claim 18, wherein the polypeptide has
2 the amino acid sequence given by any of Sequence ID Nos. 14, 16, 18, 20, 22, 24, 26, 28, 30,
3 32, 3,4 3,6 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80,
4 82, 84, 86, 88, 90, 92 or 94.